

## Sequence Table

## (2) INFORMATION FOR SEQ ID NO: 1:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382
- (B) TYPE: Amino acid
- (D) TOPOLOGY: Linear
- (ii) SEQUENCE KIND: Protein
- 10 (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Liver
- 15 (D) CLONE NAME: HP01263

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Gly Leu Leu Leu Pro Leu Ala Leu Cys Ile Leu Val Leu Cys Cys  
 20 1 5 10 15  
 Gly Ala Met Ser Pro Pro Gln Leu Ala Leu Asn Pro Ser Ala Leu Leu  
 20 25 30  
 Ser Arg Gly Cys Asn Asp Ser Asp Val Leu Ala Val Ala Gly Phe Ala  
 35 40 45  
 25 Leu Arg Asp Ile Asn Lys Asp Arg Lys Asp Gly Tyr Val Leu Arg Leu  
 50 55 60  
 Asn Arg Val Asn Asp Ala Gln Glu Tyr Arg Arg Gly Gly Leu Gly Ser  
 65 70 75 80  
 Leu Phe Tyr Leu Thr Leu Asp Val Leu Glu Thr Asp Cys His Val Leu  
 30 85 90 95  
 Arg Lys Lys Ala Trp Gln Asp Cys Gly Met Arg Ile Phe Phe Glu Ser  
 100 105 110  
 Val Tyr Gly Gln Cys Lys Ala Ile Phe Tyr Met Asn Asn Pro Ser Arg  
 115 120 125  
 35 Val Leu Tyr Leu Ala Ala Tyr Asn Cys Thr Leu Arg Pro Val Ser Lys  
 130 135 140  
 Lys Lys Ile Tyr Met Thr Cys Pro Asp Cys Pro Ser Ser Ile Pro Thr  
 145 150 155 160

	Asp	Ser	Ser	Asn	His	Gln	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	
						165					170					175	
	Lys	Tyr	Asn	Asn	Glu	Asn	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	
					180				185				190				
5	Thr	Arg	Ala	Ser	Ser	Gln	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	
			195					200				205					
	Tyr	Leu	Ile	Lys	Glu	Ser	Pro	Cys	Thr	Lys	Ser	Gln	Ala	Ser	Ser	Cys	
			210				215					220					
	Ser	Leu	Gln	Ser	Ser	Asp	Ser	Val	Pro	Val	Gly	Leu	Cys	Lys	Gly	Ser	
10	225					230					235					240	
	Leu	Thr	Arg	Thr	His	Trp	Glu	Lys	Phe	Val	Ser	Val	Thr	Cys	Asp	Phe	
					245					250					255		
	Phe	Glu	Ser	Gln	Ala	Pro	Ala	Thr	Gly	Ser	Glu	Asn	Ser	Ala	Val	Asn	
					260				265					270			
15	Gln	Lys	Pro	Thr	Asn	Leu	Pro	Lys	Val	Glu	Glu	Ser	Gln	Gln	Lys	Asn	
					275			280					285				
	Thr	Pro	Pro	Thr	Asp	Ser	Pro	Ser	Lys	Ala	Gly	Pro	Arg	Gly	Ser	Val	
					290			295				300					
	Gln	Tyr	Leu	Pro	Asp	Leu	Asp	Asp	Lys	Asn	Ser	Gln	Glu	Lys	Gly	Pro	
20	305					310					315					320	
	Gln	Glu	Ala	Phe	Pro	Val	His	Leu	Asp	Leu	Thr	Thr	Asn	Pro	Gln	Gly	
					325					330					335		
	Glu	Thr	Leu	Asp	Ile	Ser	Phe	Leu	Phe	Leu	Glu	Pro	Met	Glu	Glu	Lys	
				340					345					350			
25	Leu	Val	Val	Leu	Pro	Phe	Pro	Lys	Glu	Lys	Ala	Arg	Thr	Ala	Glu	Cys	
				355				360					365				
	Pro	Gly	Pro	Ala	Gln	Asn	Ala	Ser	Pro	Leu	Val	Leu	Pro	Pro			
				370				375					380				

30

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

35

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Trp Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His  
 1 5 10 15

10 Trp Tyr Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val  
 20 25 30

Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln  
 35 40 45

Leu Asp Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys  
 15 50 55 60

Gly Ala Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val  
 65 70 75 80

Thr Leu Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp  
 85 90 95

20 Val Lys Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn  
 100 105 110

Ala Gly Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu  
 115 120 125

Asp Ser Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val  
 25 130 135 140

Thr Leu Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val  
 145 150 155 160

Asn Val Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr  
 165 170 175

30 Cys Val Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg  
 180 185 190

Glu Ile Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr  
 195 200 205

Phe Arg Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys  
 35 210 215 220

Gln Ser Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln  
 225 230 235 240

Gln Tyr Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn

10

## (1) SEQUENCE CHARACTERISTICS:

15

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01347

25 (xi) SEQUENCE DESCRIPTION: SEO ID NO: 3:

Met	Ser	Asp	Ser	Lys	Glu	Pro	Arg	Val	Gln	Gln	Leu	Gly	Leu	Leu	Gly
1				5					10					15	
Cys	Leu	Gly	His	Gly	Ala	Leu	Val	Leu	Gln	Leu	Leu	Ser	Phe	Met	Leu
			20					25					30		
Leu	Ala	Gly	Val	Leu	Val	Ala	Ile	Leu	Val	Gln	Val	Ser	Lys	Val	Pro
			35				40					45			
Ser	Ser	Leu	Ser	Gln	Glu	Gln	Ser	Glu	Gln	Asp	Ala	Ile	Tyr	Gln	Asn
	50					55					60				
Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly	Glu	Leu	Ser	Glu	Lys	Ser	Lys
65					70					75				80	
Leu	Gln	Glu	Ile	Tyr	Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Ala	Val	Gly
				85					90					95	

Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr  
                                 100                                105                                110  
 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln  
                                 115                                120                                125  
 5 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu  
                                 130                                135                                140  
 Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu  
                                 145                                150                                155                                160  
 Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile  
 10                                  165                                170                                175  
 Tyr Gln Glu Leu Thr Glu Leu Lys Ala Ala Val Gly Glu Leu Pro Glu  
                                 180                                185                                190  
 Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala  
                                 195                                200                                205  
 15 Ala Val Gly Glu Leu Pro Asp Gln Ser Lys Gln Gln Gln Ile Tyr Gln  
                                 210                                215                                220  
 Glu Leu Thr Asp Leu Lys Thr Ala Phe Glu Arg Leu Cys Arg His Cys  
                                 225                                230                                235                                240  
 Pro Lys Asp Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn  
 20                                  245                                250                                255  
 Ser Gln Arg Asn Trp His Asp Ser Val Thr Ala Cys Gln Glu Val Arg  
                                 260                                265                                270  
 Ala Gln Leu Val Val Ile Lys Thr Ala Glu Glu Gln Leu Pro Ala Val  
                                 275                                280                                285  
 25 Leu Glu Gln Trp Arg Thr Gln Gln  
                                 290                                295

## (2) INFORMATION FOR SEQ ID NO: 4:

## 30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

## 35 (iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

5

Met Cys Thr Gly Lys Cys Ala Arg Cys Val Gly Leu Ser Leu Ile Thr  
 1 5 10 15  
 Leu Cys Leu Val Cys Ile Val Ala Asn Ala Leu Leu Leu Val Pro Asn  
 20 25 30  
 10 Gly Glu Thr Ser Trp Thr Asn Thr Asn His Leu Ser Leu Gln Val Trp  
 35 40 45  
 Leu Met Gly Gly Phe Ile Gly Gly Gly Leu Met Val Leu Cys Pro Gly  
 50 55 60  
 Ile Ala Ala Val Arg Ala Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys  
 15 65 70 75 80  
 Cys Gly Asn Arg Cys Arg Met Leu Arg Ser Val Phe Ser Ser Ala Phe  
 85 90 95  
 Gly Val Leu Gly Ala Ile Tyr Cys Leu Ser Val Ser Gly Ala Gly Leu  
 100 105 110  
 20 Arg Asn Gly Pro Arg Cys Leu Met Asn Gly Glu Trp Gly Tyr His Phe  
 115 120 125  
 Glu Asp Thr Ala Gly Ala Tyr Leu Leu Asn Arg Thr Leu Trp Asp Arg  
 130 135 140  
 Cys Glu Ala Pro Pro Arg Val Val Pro Trp Asn Val Thr Leu Phe Ser  
 25 145 150 155 160  
 Leu Leu Val Ala Ala Ser Cys Leu Glu Ile Val Leu Cys Gly Ile Gln  
 165 170 175  
 Leu Val Asn Ala Thr Ile Gly Val Phe Cys Gly Asp Cys Arg Lys Lys  
 180 185 190  
 30 Gln Asp Thr Pro His  
 195

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 221

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 5 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP01526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

10 Met Glu Ala Gly Gly Phe Leu Asp Ser Leu Ile Tyr Gly Ala Cys Val
    1           5           10           15
Val Phe Thr Leu Gly Met Phe Ser Ala Gly Leu Ser Asp Leu Arg His
    20           25           30
Met Arg Met Thr Arg Ser Val Asp Asn Val Gln Phe Leu Pro Phe Leu
15    35           40           45
Thr Thr Glu Val Asn Asn Leu Gly Trp Leu Ser Tyr Gly Ala Leu Lys
    50           55           60
Gly Asp Gly Ile Leu Ile Val Val Asn Thr Val Gly Ala Ala Leu Gln
    65           70           75           80
20 Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr Cys Pro Arg Lys Arg Val
    85           90           95
Val Leu Leu Gln Thr Ala Thr Leu Leu Gly Val Leu Leu Leu Gly Tyr
    100          105          110
Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro Glu Ala Arg Leu Gln Gln
25    115          120          125
Leu Gly Leu Phe Cys Ser Val Phe Thr Ile Ser Met Tyr Leu Ser Pro
    130          135          140
Leu Ala Asp Leu Ala Lys Val Ile Gln Thr Lys Ser Thr Gln Cys Leu
    145          150          155          160
30 Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu Thr Ser Ala Ser Trp Cys
    165          170          175
Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr Ile Met Val Ser Asn Phe
    180          185          190
Pro Gly Ile Val Thr Ser Phe Ile Arg Phe Trp Leu Phe Trp Lys Tyr
35    195          200          205
Pro Gln Glu Gln Asp Arg Asn Thr Trp Leu Leu Gln Thr
    210          215          220

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## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251

(B) TYPE: Amino acid

5 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

10 (A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

15

```

Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala Ile Thr Arg
 1             5             10             15
Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys Leu Gly
      20             25             30
20 Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala Phe Leu Tyr
      35             40             45
Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr Phe Pro Val
 50             55             60
Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr Phe Leu Tyr
25 65             70             75             80
Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly Arg Pro Ala
      85             90             95
Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile Val Ile Thr
      100            105            110
30 Gly Leu Ala Met Asp Met Gln Leu Leu Met Ile Pro Leu Ile Met Ser
      115            120            125
Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile Val Ser Phe
      130            135            140
Trp Gly Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp Val Ile Leu
35 145            150            155            160
Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu Leu Ile Gly
      165            170            175
Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg Tyr Pro Met

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(i) SEQUENCE CHARACTERISTICS:

15

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10389

## 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met	Ala	Thr	Pro	Gly	Pro	Val	Ile	Pro	Glu	Val	Pro	Phe	Glu	Pro	Ser
1				5					10					15	
Lys	Pro	Pro	Val	Ile	Glu	Gly	Leu	Ser	Pro	Thr	Val	Tyr	Arg	Asn	Pro
			20					25					30		
Glu	Ser	Phe	Lys	Glu	Lys	Phe	Val	Arg	Lys	Thr	Arg	Glu	Asn	Pro	Val
			35					40					45		
Val	Pro	Ile	Gly	Cys	Leu	Ala	Thr	Ala	Ala	Ala	Leu	Thr	Tyr	Gly	Leu
			50				55				60				
Tyr	Ser	Phe	His	Arg	Gly	Asn	Ser	Gln	Arg	Ser	Gln	Leu	Met	Met	Arg
			65			70					75				80
Thr	Arg	Ile	Ala	Ala	Gln	Gly	Phe	Thr	Val	Ala	Ala	Ile	Leu	Leu	Gly

Leu Ala Val Thr Ala Met Lys Ser Arg Pro  
 100 105

5

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78

10 (B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

15 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10408

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly Ser  
 1 5 10 15  
 Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu Lys Glu  
 25 20 25 30  
 Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu Glu Leu Leu  
 35 40 45  
 Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly Thr Ser Val Thr  
 50 55 60  
 30 Leu His His Ala Arg Ser Gln His His Val Val Cys Asn Thr  
 65 70 75

## (2) INFORMATION FOR SEQ ID NO: 9:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

10

```

Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly
  1             5             10             15
Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
             20             25             30
15 Gln Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala
             35             40             45
Gln Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro
             50             55             60
Arg Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala
20 65             70             75             80
Gln Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val
             85             90             95
Ile Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His
             100            105            110
25 Leu Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys
             115            120            125
Gln Ala Arg Lys Ala Gln Arg Glu Glu Ala Glu Arg Glu Glu
             130            135            140
Arg Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu
30 145            150            155            160
Glu Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys
             165            170            175
Ala Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu
             180            185            190
35 Lys Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr
             195            200            205
Glu Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys
             210            215            220

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[illegible]

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 195

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

## 20 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

30 Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala Asp Pro Ser Asp Leu  
1 5 10 15  
Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr Ser Pro Leu Asn Leu  
20 25 30  
Leu Leu Leu Gly Leu Cys Ile Phe Leu Leu Tyr Lys Ile Val Arg Gly  
35 35 40 45  
Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp Asp Glu Pro Pro Pro  
50 55 60  
Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro Ala Glu Leu Arg Arg



9. 2010

(A) LENGTH: 462

(A) ORGANISM: *Homo sapiens*

(iii) HYPOTHETICAL: No

(A) ORGANISM: *Homo sapiens*

30

10

Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile  
 35 40 45  
 Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn Leu His Glu Arg  
 50 55 60  
 5 Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser  
 65 70 75 80  
 Leu Gly Thr Val Asp Val Leu Lys Gln His Ile Asn Pro Asn Lys Thr  
 85 90 95  
 Leu Asp Pro Phe Glu Thr Met Leu Lys Ser Leu Leu Arg Tyr Gln Ser  
 10 100 105 110  
 Gly Gly Gly Ser Val Ser Glu Asn His Met Arg Lys Lys Leu Tyr Glu  
 115 120 125  
 Asn Gly Val Thr Asp Ser Leu Lys Ser Asn Phe Ala Leu Leu Leu Lys  
 130 135 140  
 15 Leu Ser Glu Glu Leu Leu Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln  
 145 150 155 160  
 His Val Pro Leu Ser Gln His Met Leu Gly Phe Ala Met Lys Ser Val  
 165 170 175  
 Thr Gln Met Val Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile  
 20 180 185 190  
 Arg Phe Gln Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly  
 195 200 205  
 Phe Leu Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr  
 210 215 220  
 25 Glu Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys  
 225 230 235 240  
 Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser Leu  
 245 250 255  
 Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser Met Ile  
 30 260 265 270  
 Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys Thr Trp Ala  
 275 280 285  
 Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys Lys Leu Tyr Glu  
 290 295 300  
 35 Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val Thr Pro Glu Lys Ile  
 305 310 315 320  
 Glu Gln Leu Arg Tyr Cys Gln His Val Leu Cys Glu Thr Val Arg Thr  
 325 330 335

Ala Lys Leu Thr Pro Val Ser Ala Gln Leu Gln Asp Ile Glu Gly Lys  
 340 345 350  
 Ile Asp Arg Phe Ile Ile Pro Arg Glu Thr Leu Val Leu Tyr Ala Leu  
 355 360 365  
 5 Gly Val Val Leu Gln Asp Pro Asn Thr Trp Pro Ser Pro His Lys Phe  
 370 375 380  
 Asp Pro Asp Arg Phe Asp Asp Glu Leu Val Met Lys Thr Phe Ser Ser  
 385 390 395 400  
 Leu Gly Phe Ser Gly Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr  
 10 405 410 415  
 Met Val Thr Thr Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu  
 420 425 430  
 Leu Ser Val Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr  
 435 440 445  
 15 Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO: 12:

## 20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

## 25 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

## 30 (D) CLONE NAME: HP10419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro  
 35 1 5 10 15  
 Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu Arg Val  
 20 25 30  
 Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu Leu Leu

	35		40		45
	Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg Ser Asp				
	50		55		60
	Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val Ser Val				
5	65		70		75
	Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu Lys Lys				
		85		90	95
	Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser Pro Ile				
		100		105	110
10	Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly Ile Ile				
		115		120	125
	Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu Gly Pro				
		130		135	140
	Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu Thr Ser				
15	145		150		155
	Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp Gly Val				
		165		170	175
	Val Phe Phe Asp Ala Cys Glu Arg Arg Tyr Trp Ala Leu Gly Leu				
		180		185	190
20	Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu Asn Pro				
		195		200	205
	Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val Ser Met				
		210		215	220
	Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln				
25	225		230		235
	Arg Ser Leu Leu Cys Lys Asp				240
		245			

30 (2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

35 (ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:



(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10424

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
  1           5           10           15
Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
10          20          25          30
Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
  35          40          45
Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
  50          55          60
15 Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
  65          70          75          80
Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
          85          90          95
Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
20          100          105          110
Thr

```

(2) INFORMATION FOR SEQ ID NO: 14:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365  
 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

30 (iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Epidermoid carcinoma  
 (C) CELL LINE: KB  
 (D) CLONE NAME: HP10428

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu  
 1 5 10 15  
 Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr  
 20 25 30  
 5 Phe Tyr Asn Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met  
 35 40 45  
 Thr Met Leu His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg  
 50 55 60  
 Ala Leu Val Gln Cys Ser Ser His Arg Ala Arg Val Val Leu Ser Trp  
 10 65 70 75 80  
 Ala Asp Tyr Leu Arg Arg Val Ala Pro Thr Ala Leu Ala Thr Ala Leu  
 85 90 95  
 Asp Val Gly Leu Ser Asn Trp Ser Phe Leu Tyr Val Thr Val Ser Leu  
 100 105 110  
 15 Tyr Thr Met Thr Lys Ser Ser Ala Val Leu Phe Ile Leu Ile Phe Ser  
 115 120 125  
 Leu Ile Phe Lys Leu Glu Glu Leu Arg Ala Ala Leu Val Leu Val Val  
 130 135 140  
 Leu Leu Ile Ala Gly Gly Leu Phe Met Phe Thr Tyr Lys Ser Thr Gln  
 20 145 150 155 160  
 Phe Asn Val Glu Gly Phe Ala Leu Val Leu Gly Ala Ser Phe Ile Gly  
 165 170 175  
 Gly Ile Arg Trp Thr Leu Thr Gln Met Leu Leu Gln Lys Ala Glu Leu  
 180 185 190  
 25 Gly Leu Gln Asn Pro Ile Asp Thr Met Phe His Leu Gln Pro Leu Met  
 195 200 205  
 Phe Leu Gly Leu Phe Pro Leu Phe Ala Val Phe Glu Gly Leu His Leu  
 210 215 220  
 Ser Thr Ser Glu Lys Ile Phe Arg Phe Gln Asp Thr Gly Leu Leu Leu  
 30 225 230 235 240  
 Arg Val Leu Gly Ser Leu Phe Leu Gly Gly Ile Leu Ala Phe Gly Leu  
 245 250 255  
 Gly Phe Ser Glu Phe Leu Leu Val Ser Arg Thr Ser Ser Leu Thr Leu  
 260 265 270  
 35 Ser Ile Ala Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala  
 275 280 285  
 His Leu Leu Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala  
 290 295 300

Leu Cys Leu Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His  
 305 310 315 320  
 Ser Arg Gly Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser  
 325 330 335  
 5 Pro Asp Leu Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp  
 340 345 350  
 Asn Glu Glu Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln  
 355 360 365

10

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226

(B) TYPE: Amino acid

15

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

## (vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10429

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

25

Met Pro Thr Thr Lys Lys Thr Leu Met Phe Leu Ser Ser Phe Phe Thr  
 1 5 10 15  
 Ser Leu Gly Ser Phe Ile Val Ile Cys Ser Ile Leu Gly Thr Gln Ala  
 20 25 30  
 30 Trp Ile Thr Ser Thr Ile Ala Val Arg Asp Ser Ala Ser Asn Gly Ser  
 35 40 45  
 Ile Phe Ile Thr Tyr Gly Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu  
 50 55 60  
 Ser His Gly Leu Ala Glu Pro Lys Lys Lys Phe Ala Val Leu Glu Ile  
 35 65 70 75 80  
 Leu Asn Asn Ser Ser Gln Lys Thr Leu His Ser Val Thr Ile Leu Phe  
 85 90 95  
 Leu Val Leu Ser Leu Ile Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe



35 Met Ala Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly  
1 5 10 15  
Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly  
20 25 30

Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys  
 35 40 45  
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys  
 50 55 60  
 5 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro  
 65 70 75 80  
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser  
 85 90 95  
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr  
 10 100 105 110  
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile  
 115 120 125  
 Gln

15

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163

20

(B) TYPE: Amino acid

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: Protein

(iii) HYPOTHETICAL: No

25

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP10433

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly  
 1 5 10 15  
 Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val  
 35 20 25 30  
 Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln  
 35 40 45  
 Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile

50                      55                      60  
 Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg  
 65                      70                      75                      80  
 Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg  
 5                      85                      90                      95  
 Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly  
 100                      105                      110  
 Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu  
 115                      120                      125  
 10 Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp  
 130                      135                      140  
 Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu  
 145                      150                      155                      160  
 Pro Arg Ser  
 15

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193  
 20 (B) TYPE: Amino acid  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: Protein  
 (iii) HYPOTHETICAL: No

## 25 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10480

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro  
 1                      5                      10                      15  
 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly  
 35                      20                      25                      30  
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp  
 35                      40                      45  
 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

	50		55		60											
	Cys	Gln	Ser	Leu	Met	Glu	Tyr	Ala	Trp	Gly	Arg	Ala	Ala	Ala	Ala	Met
	65					70				75						80
	Leu	Phe	Cys	Gly	Phe	Ile	Ile	Leu	Val	Ile	Cys	Phe	Ile	Leu	Ser	Phe
5						85				90						95
	Phe	Ala	Leu	Cys	Gly	Pro	Gln	Met	Leu	Val	Phe	Leu	Arg	Val	Ile	Gly
						100				105					110	
	Gly	Leu	Leu	Ala	Leu	Ala	Ala	Val	Phe	Gln	Ile	Ile	Ser	Leu	Val	Ile
						115				120					125	
10	Tyr	Pro	Val	Lys	Tyr	Thr	Gln	Thr	Phe	Thr	Leu	His	Ala	Asn	Arg	Ala
						130				135					140	
	Val	Thr	Tyr	Ile	Tyr	Asn	Trp	Ala	Tyr	Gly	Phe	Gly	Trp	Ala	Ala	Thr
						145				150				155		160
	Ile	Ile	Leu	Ile	Gly	Cys	Ala	Phe	Phe	Phe	Cys	Cys	Leu	Pro	Asn	Tyr
15						165				170					175	
	Glu	Asp	Asp	Leu	Leu	Gly	Asn	Ala	Lys	Pro	Arg	Tyr	Phe	Tyr	Thr	Ser
						180				185					190	
	Ala															

20

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146

(B) TYPE: Nucleic acid

25

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

30

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Linear

(D) CLONE NAME: HP01263

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

35

ATGGGTCTGC	TCCTTCCCT	GGCACTCTGC	ATCCTAGTCC	TGTGCTGCGG	AGCAATGTCT	60
CCACCCCAGC	TGGCCCTCAA	CCCCTCGGCT	CTGCTCTCCC	GGGGCTGCAA	TGACTCCGAT	120
GTGCTGGCAG	TTGCAGGCTT	TGCCCTGCGG	GATATTAACA	AAGACAGAAA	GGATGGCTAT	180

```

GTGCTGAGAC TCAACCGAGT GAACGACGCC CAGGAATACA GACGGGGTGG CCTGGGATCT 240
CTGTTCTATC TTACACTGGA TGTGCTAGAG ACTGACTGCC ATGTGCTCAG AAAGAAGGCA 300
TGGCAAGACT GTGGAATGAG GATATTTTTT GAATCAGTTT ATGGTCAATG CAAAGCAATA 360
TTTTATATGA ACAACCCAAAG TAGAGTTCTC TATTTAGCTG CTTATAACTG TACTCTTCGC 420
5 CCAGTTTCAA AAAAAAAGAT TTACATGACG TGCCCTGACT GCCCAAGCTC CATACCCACT 480
GACTCTTCCA ATCACCAGT GCTGGAGGCT GCCACCGAGT CTCTTGCGAA ATACAACAAT 540
GAGAACACAT CCAAGCAGTA TTCTCTCTTC AAAGTCACCA GGGCTTCTAG CCAGTGGGTG 600
GTGGGCCCTT CTTACTTTGT GGAATACTTA ATTAAGAAT CACCATGTAC TAAATCCAG 660
GCCAGCAGCT GTTCACTTCA GTCCTCCGAC TCTGTGCTG TTGGTCTTTG CAAAGGTTCT 720
10 CTGACTCGAA CACACTGGGA AAAGTTTGTG TCTGTGACTT GTGACTTCTT TGAATCACAG 780
GCTCCAGCCA CTGGAAGTGA AAAGTCTGCT GTTAACCAGA AACCTACAAA CCTTCCCAAG 840
GTGGAAGAAT CCCAGCAGAA AAACACCCCC CCAACAGACT CCCCTCCAA AGCTGGGCCA 900
AGAGGATCTG TCCAATATCT TCTGACTTG GATGATAAAA ATTCCCAGGA AAAGGGCCCT 960
CAGGAGGCCT TTCCTGTGCA TCTGGACCTA ACCACGAATC CCCAGGGAGA AACCTGGAT 1020
15 ATTTCTTCC TCTTCCTGGA GCCTATGGAG GAGAAGCTGG TTGTCTGCC TTTCCCCAAA 1080
GAAAAAGCAC GCAGTGCTGA GTGCCAGGG CCAGCCAGA ATGCCAGCC TCTGTCTCTT 1140
CCGCCA 1146

```

20 (2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 951
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

25

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Liver
- (D) CLONE NAME: HP01299

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```

35 ATGTGGCTCT ACCTGGCGGC CTTCGTGGGC CTGTACTACC TTCTGCACTG GTACCGGGAG 60
AGGCAGGTGG TGAGCCACCT CCAAGACAAG TATGTCTTTA TCACGGGCTG TGACTCGGGC 120
TTTGGGAACC TGCTGGCCAG ACAGCTGGAT GCACGAGGCT TGAGATGCT GCCTGCGTGT 180
CTGACGGAGA AGGGGGCCGA GCAGCTGAGG GGCCAGACGT CTGACAGGCT GGAGACGGT 240

```



	ACCCTGGATG	TIACCAAGAT	GGAGAGCATC	GCTGCAGCTA	CTCAGTGGGT	GAAGGAGCAT	300
	GTGGGGGACA	GAGGACTCTG	GGGACTGGTG	AACAATGCAG	GCATTCTTAC	ACCAATTACC	360
	TTATGTGAGT	GGCTGAACAC	TGAGGACTCT	ATGAATATGC	TCAAAGTGAA	CCTCATTGGT	420
	GTGATCCAGG	TGACCTTGAG	CATGCTTCCT	TTGGTGAGGA	GAGCACGGGG	AAGAATTGTC	480
5	AATGTCTCCA	GCATTCTGGG	AAGAGTTGCT	TTCTTTGTAG	GAGGCTACTG	TGTCTCCAAG	540
	TATGGAGTGG	AAGCCTTTTC	AGATATTCTG	AGGCGTGAGA	TTCAACATTT	TGGGGTGAAA	600
	ATCAGCATAG	TTGAACCTGG	CTACTTCAGA	ACGGGAATGA	CAAACATGAC	ACAGTCCTTA	660
	GAGCGAATGA	AGCAAAGTTG	GAAGAAGGCC	CCCAAGCATA	TTAAGGAGAC	CTATGGACAG	720
	CAGTATTTTG	ATGCCCTTTA	CAATATCATG	AAGGAAGGGC	TGTTGAATTG	TAGCACAAAC	780
10	CTGAACCTGG	TCACTGACTG	CATGGAACAT	GCTCTGACAT	CGGTGCATCC	GCGAACTCGA	840
	TATTCAGCTG	GCTGGGATGC	TAAATTTTTC	TTCATCCCTC	TATCTTATTT	ACCTACATCA	900
	CTGGCAGACT	ACATTTTGAC	TAGATCTTGG	CCCAAACCAG	CCCAGGCAGT	C	951

15 (2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 888

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP01347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

30	ATGAGTGACT	CCAAGGAACC	AAGGGTGCAG	CAGCTGGGCC	TCCTGGGGTG	TCTTGGCCAT	60
	GGCGCCTTGG	TGCTGCAACT	CCTCTCCTTC	ATGCTCTTGG	CTGGGGTCCT	GGTGGCCATC	120
	CTTGTCCAAG	TGTCCAAGGT	CCCCAGCTCC	CTAAGTCAGG	AACAATCCGA	GCAAGACGCA	180
	ATCTACCAGA	ACCTGACCCA	GCTTAAAGCT	GCAGTGGGTG	AGCTCTCAGA	GAAATCCAAG	240
	CTGCAGGAGA	TCTACCAGGA	GCTGACCCAG	CTGAAGGCTG	CAGTGGGTGA	GTTGCCAGAG	300
35	AAATCCAAGC	TGCAGGAGAT	CTACCAGGAG	CTGACCCGGC	TGAAGGCTGC	AGTGGGTGAG	360
	TTGCCAGAGA	AATCCAAGCT	GCAGGAGATC	TACCAGGAGC	TGACCCGGGT	GAAGGCTGCA	420
	GTGGGTGAGT	TGCCAGAGAA	ATCCAAGCTG	CAGGAGATCT	ACCAGGAGCT	GACCCGGCTG	480
	AAGGCTGCAG	TGGGTGAGTT	GCCAGAGAAA	TCCAAGCTGC	AGGAGATCTA	CCAGGAGCTG	540

	ACGGAGCTGA AGGCTGCAGT GGGTGAGTTG CCAGAGAAAT CCAAGCTGCA GGAGATCTAC	600
	CAGGAGCTGA CCCAGCTGAA GGCTGCAGTG GGTGAGTTGC CAGACCACTC CAAGCAGCAG	660
	CAAACTCTATC AAGAACTGAC CGATTGGAAG ACTGCATTGT AACGCCTGTG CCGCCACTGT	720
	CCCAAGGACT GGACATTCTT CCAAGGAAAC TGTTACTTCA TGCTCTAACT CCAGCGGAAC	780
5	TGGCAGGACT CCGTCACCGC CTGCCAGGAA GTGAGGGCCC AGTCGTCGT AATCAAAACT	840
	GCTGAGGAGC AGCTTCCAGC GGTACTGGAA CAGTGGAGAA CCCAACAA	888

## (2) INFORMATION FOR SEQ ID NO: 22:

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 15 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer

## 20 (D) CLONE NAME: HP01440

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

	ATGTGTACGG GAAAATGTC CCGCTGTGTG GGGCTCTCCC TCATTACCCT CTGCCTCGTC	60
25	TGCATTGTGG CCAACGCCCT CCGCTGTGTA CCTAATGGGG AGACCTCCTG GACCAACACC	120
	AACCATCTCA GCTTGCAAGT CTGGCTCATG GCGGGCTTCA TTGGCGGGGG CCTAATGGTA	180
	CTGTGTCCGG GGATTGCAGC CGTTCCGGCA GGGGCAAGG GCTGCTGTGG TGCTGGGTGC	240
	TGTGGAAACC GCTGCAGGAT GCTGCGCTCG GTCTTCTCCT CGGCGTTCGG GGTGCTTGTT	300
	GCCATCTACT GCCTCTCGGT GTCTGGAGCT GGGCTCCGAA ATGGACCCAG ATGCTTAATG	360
30	AACGGCGAGT GGGGCTACCA CTTGCAAGAC ACCGCGGGAG CTTACTTGCT CAACCGCACT	420
	CTATGGGATC GGTGCGAGGC GCCCCTCGC GTGGTCCCTT GGAATGTGAC GCTCTTCTCG	480
	CTGCTGGTGG CCGCCTCCTG CCGTGGAGATA GTACTGTGTG GGATCCAGCT GGTGAACGCG	540
	ACCATTTGGT TCTTCTGCGG CGATTGCAGG AAAAAACAGG ACACCCCTCA C	591

35

## (2) INFORMATION FOR SEQ ID NO: 23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663

(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP01526

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

ATGGAGGCGG	GCGGCTTTCT	GGA	CTCGCTC	ATTTACGGAG	CATGCGTGGT	CTTCACCCCTT	60
GGCATGTTCT	CCGCCGGCCT	CTCGGACCTC	AGGCACATGC	GAATGACCCG	GAGTGTGGAC		120
15 AACGTCAGT	TCCTGCCCTT	TCTCACCACG	GAAGTCAACA	ACCTGGGCTG	GCTGAGTTAT		180
GGGGCTTTGA	AGGGAGACGG	GATCCTCATC	GTCTCAACA	CAGTGGGTGC	TGCGCTTCAG		240
ACCCTGTATA	TCTTGGCATA	TCTGCATTAC	TGCCCTCGGA	AGCGTGTGT	GCTCCTACAG		300
ACTGCAACCC	TGCTAGGGGT	CCTTCTCCTG	GGTTATGGCT	ACTTTTGGCT	CCTGGTACCC		360
AACCCTGAGG	CCCGGCTTCA	GCAGTTGGGC	CTCTTCTGCA	GTGTCTTAC	CATCAGCATG		420
20 TACCTCTCAC	CACTGGCTGA	CTTGGCTAAG	GTGATTCAAA	CTAAATCAAC	CCAATGTCTC		480
TCCTACCCAC	TCACCATTCG	TACCCTTCTC	ACCTCTGCCT	CCTGGTGCCT	CTATGGGTTT		540
CGACTCAGAG	ATCCCTATAT	CATGGTGTCC	AACTTTCAG	GAATCGTCAC	CAGCTTTATC		600
CGCTTCTGGC	TTTCTGGAA	GTACCCCCAG	GAGCAAGACA	GGAACACTGT	GCTCCTGCAA		660
ACC							663

25

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 753  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

30

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10230

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

	ATGTCGGACA	TCGGAGACTG	GTTCAGGAGC	ATCCCGGCGA	TCACGCGCTA	TTGGTTGGCC	60
	GCCACCGTCG	CGGTGCCCTT	GGTCGGCAAA	CTCGGCCTCA	TCAGCCCGGC	CTACCTCTTC	120
5	CTCTGGCCCG	AAGCCTTCT	TTATCGCTTT	CAGATTGGA	GGCCAATCAC	TGCCACCTTT	180
	TATTTCCCTG	TGGGTCCAGG	AACGGATT	CTTTATTGG	TCAATTTATA	TTTCTTATAT	240
	CAGTATTCTA	CGCGACTTGA	AACAGGAGCT	TTTGATGGGA	GGCCAGCAGA	CTATTTATTC	300
	ATGCTCCTCT	TTAACTGGAT	TTGCATCGTG	ATTACTGGCT	TAGCAATGGA	TATGCAGTTG	360
	CTGATGATTC	CTCTGATCAT	GTCACTACTT	TATGTCTGGG	CCCAGCTGAA	CAGAGACATG	420
10	ATTGTATCAT	TTTGGTTTGG	AACAGGATT	AAGGCCTGCT	ATTACCCCTG	GGTTATCCTT	480
	GGATTCAACT	ATATCATCGG	AGGCTCGGTA	ATCAATGAGC	TTATTGGAAA	TCTGGTTGGA	540
	CATCTTTATT	TTTTCTTAAT	GTTCAAGTAC	CCAATGGACT	TGGGAGGAAG	AAATTTTCTA	600
	TCCACACCTC	AGTTTTTGTA	CCGCTGGCTG	CCCAGTAGGA	GAGGAGGAGT	ATCAGGATTT	660
	GGTGTGCCCC	CTGTAGCAT	GAGGCGAGCT	GCTGATCAGA	ATGGCGGAGG	CGGGAGACAC	720
15	AACTGGGGCC	AGGGCTTTCG	ACTTGGAGAC	CAG			753

## (2) INFORMATION FOR SEQ ID NO: 25:

## (i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 318
	(B) TYPE: Nucleic acid
	(C) STRANDEDNESS: Double
	(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

25

## (vi) ORIGINAL SOURCE:

	(A) ORGANISM: <i>Homo sapiens</i>
	(B) CELL KIND: Epidermoid carcinoma
	(C) CELL LINE: KB
30	(D) CLONE NAME: HP10389

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

	ATGGCGACTC	CGGGCCCTGT	GATTCCGGAG	GTCCCCTTTG	AACCATCGAA	GCCTCCAGTC	60
35	ATTGAGGGGC	TGAGCCCCAC	TGTTTACAGG	AATCCAGAGA	GTTTCAAGGA	AAAGTTCGTT	120
	CGCAAGACCC	GCGAGAACCC	GGTGTACCC	ATAGGTTGCC	TGGCCACGGC	GGCCGCCCTC	180
	ACCTACGGCC	TCTACTCCTT	CCACCGGGGC	AACAGCCAGC	GCTCTCAGCT	CATGATGCGC	240
	ACCCGGATCG	CGGCCAGGG	TTTCACGGTC	GCAGCCATCT	TGCTGGGTCT	GGCTGTCACT	300

GCTATGAAGT CTCGACCC

318

## (2) INFORMATION FOR SEQ ID NO: 26:

## 5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 10 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer

## 15 (D) CLONE NAME: HP10408

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATGGGGTCTG	GGCTGCCCT	TGCTCTCTC	TTGACCTCC	TTGGCAGCTC	ACATGGAACA	60
20	GGGCCGGGTA	TGACTTTGCA	ACTGAAGCTG	AAGGAGTCTT	TTCTGACAAA	120
	GAGTCCAGCT	TCCTGGAATT	GCTTGAAAAG	CTCTGCCTCC	TCCTCCATCT	180
	ACCAGCGTCA	CCCTCCACCA	TGCAAGATCT	CAACACCATG	TTGTCTGCAA	234
				CACA		

## 25 (2) INFORMATION FOR SEQ ID NO: 27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 942
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 30 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10412

## 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

ATGGTGGCGC CTGTGTGTA CTTGGTAGCG GCGGCTCTGC TAGTCGGCTT TATCCTCTTC      60
CTGACTCGCA GCCGGGGCCG GCGGGCATCA GCCGGCCAAG AGCCACTGCA CAATGAGGAG      120
CTGGCAGGAG CAGGGCCGGT GCCCAGCCT GGGCCCTTGG AGCCTGAGGA GCCGAGAGCT      180
GGAGGCAGGC CTCGGCGCCG GAGGGACCTG GGCAGCCGCC TACAGGCCCA CGCTCGAGCC      240
5  CAGCGGGTGG CCTGGGCAGA AGCAGATGAG AACGAGGAGG AAGCTGTCAT CCTAGCCCCAG      300
GAGGAGGAAG GTGTGCAGAA GCCAGCGGAA ACTCACCTGT CGGGGAAAAT TGGAGCTAAG      360
AAACTGCGGA AGCTGGAGGA GAAACAAGCG CGAAAGGCCG AGCGTGAGGC AGAGGAGGCT      420
GAACGTGAGG AGCGGAAACG ACTCGAGTCC CAGCGCGAAG CTGAGTGGA GAAGGAGGAG      480
GAGCGGCTTC GCCTGGAGGA GGAGCAGAAG GAGGAGGAGG AGAGGAAGGC CCGCGAGGAG      540
10 CAGGCCCAGC GGGAGCATGA GGAGTACCTG AAAGTGAAGG AGGCCTTTGT GGTGGAGGAG      600
GAAGGCGTAG GAGAGACCAT GACTGAGGAA CAGTCCCAGA GCTTCCTGAC AGAGTTCATC      660
AACTACATCA AGCAGTCCAA GGTGTGTGCTC TTGGAAGACC TGGCTTCCCA GGTGGGCCTA      720
CGCACTCAGG ACACCATAAA TCGCATCCAG GACCTGCTGG CTGAGGGGAC TATAACAGGT      780
GTGATTGACG ACCGGGGCAA GTTCATCTAC ATAACCCAG AGGAAGTGGC CGCCGTGGCC      840
15 AACTTCATCC GACAGCGGGG CCGGGTGTCC ATCGCCGAGC TTGCCCAAGC CAGCAACTCC      900
CTCATCGCCT GGGGCCGGGA GTCCCTTGCC CAAGCCCCAG CC      942

```

## (2) INFORMATION FOR SEQ ID NO: 28:

## 20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 25 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10413

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

```

ATGGCTGCCG AGGATGTGGT GCGCACTGCG GCGACCCAA GCGATCTGGA GAGCGGCGGG      60
35 CTGCTGCATG AGATTTTCAC GTCGCCGCTC AACCTGCTGC TGCTTGGCCT CTGCATCTTC      120
CTGCTCTACA AGATCGTSCG CGGGGACGAG CCGGCGGCCA GCGCGACAG CGACAGCAGC      180
GAGCGGCCCC CTCTGCCCGG CCTCAAGCGG CGCGACTTCA CCCCGGCCGA GCTCGGGCGC      240
TTGACGCGCG TCCAGGACCC GCGCATACTC ATGGCCATCA ACGGCAAGGT GTTCGATGTG      300

```

	ACCAAAGGCC	GCAAATTCTA	CGGGCCCGAG	GGGCGGTATG	GGGTCTTTGC	TGGAAGAGAT	360
	GCATCCAGGG	GCCTTGCCAC	ATTTTGCCTG	GATAAGGAAG	CACTGAAGGA	TGAGTACGAT	420
	GACCTTTCTG	ACCTCACTGC	TGCCCAGCAG	GAGACTCTGA	GTGACTGGGA	GTCTCAGTTC	480
	ACTTTCAAGT	ATCATCACGT	GGGCAAACTG	CTGAAGGAGG	GGGAGGAGCC	CACTGTGTAC	540
5	TCAGATGAGG	AAGAACCAAA	AGATGAGAGT	GCCCGGAAAA	ATGAT		585

## (2) INFORMATION FOR SEQ ID NO: 29:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1386  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear  
 (ii) SEQUENCE KIND: cDNA to mRNA

- 15 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10415

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

	ATGTTGGA	CTTCG	GATCTT	CGCGTT	TACC	TTCTTG	CTGG	CGTTGG	TGGG	AGCCGT	GCTC	60	
	TACCTCT	ATC	CGGCTT	CCAG	ACAAGCT	GCA	GGAAT	TCCAG	GGATT	TACTCC	AACTGA	AAGAA	120
25	AAAGAT	GGTA	ATCTT	CCAGA	TATTGT	GAA	AGTT	TGCAT	GAGTT	CCTGGT	TTAA	180	
	TTGCAT	GAGA	GATAT	GGGCC	TGTGGT	CTCC	TTCTGG	TTTG	GCAGGC	GCCT	CGTG	TTAGT	240
	TTGGGC	ACTG	TTGAT	GTACT	GAAGC	AGCAT	ATCAAT	CCCCA	ATAAG	ACATT	GGACC	CTTTT	300
	GAAACCA	TGC	TGAAG	TCA	TTAAG	GTAT	CAATC	TGGTG	GTGGC	AGTGT	GAAAA	C	360
	CACATG	AGGA	AAAAAT	TGTA	TGAAA	ATGGT	GTGACT	GATT	CTCTG	AAGAG	TAAC	TTTGGC	420
30	CTCCTC	CTAA	AGCTT	TTCAGA	AGAATT	TATTA	GATAA	TGCG	TCTC	TACCC	AGAGAC	CCAG	480
	CACGTG	CCCC	TCAGCC	AGCA	TATGCT	TGGT	TTGCT	ATGA	AGTCT	GTTAC	ACAGAT	GGTA	540
	ATGGGT	AGTA	CATTTG	AAGA	TGATC	AGAA	GTCATT	CGCT	TCCAG	AAGAA	TCATG	GCACA	600
	GTTTGG	TCTG	AGATTG	GAAA	AGGCTT	TCTA	GATGGG	TCAC	TTGATA	AAAAA	CATGAC	TCGG	660
	AAAAAA	CAAT	ATGAAG	ATGC	CCTCAT	GCAA	CTGGAG	CTCG	TTTTAA	AGGAA	CATCATA	AAAAA	720
35	GAACG	AAAAA	GAAGAA	CACTT	CAGTCA	ACAT	ATTTCA	ATTG	ACTC	CTTAGT	ACAAGG	GAAC	780
	CTTAAT	GACC	AACAGAT	TCCT	AGAAG	ACAGT	ATGAT	ATTTT	CTCTG	GCCAG	TTGCATA	AATA	840
	ACTGCA	AAAT	TGTGT	ACCTG	GGCAAT	CTGT	TTTTTA	ACCA	CCTCT	GAA	AGTTCA	AAAAA	900
	AAATTAT	ATG	AAGATA	AAAA	CCAAGT	TTTTT	GGAAAT	TGGTC	CTGTT	TACTCC	AGAGAAA	AATT	960

GAGCAGCTCA GATATTGTCA GCATGTGCTT TGTGAACTG TTCGAACTGC CAAACTGACT 1020  
 CCAGTTTCTG CCCAGCTTCA AGATATTGAA GGAAAAATTG ACCGATTAT TATTCTAGA 1080  
 GAGACCCTCG TCCTTTATGC CCTTGGTGTG TACTTCAGG ATCCTAATAC TTGGCCATCT 1140  
 CCACACAAGT TTGATCCAGA TCGGTTTGAT GATGAATTAG TAATGAAAAC TTTTCCTCA 1200  
 5 CTTGGATTCT CAGGCACACA GGAGTGTCCTA GAGTTGAGGT TTGCATATAT GGTGACCACA 1260  
 GTACTTCTTA GTGTATTGGT GAAGAGACTG CACCTACTTT CTGTGGAGGG ACAGGTTATT 1320  
 GAAACAAAGT ATGAACTGGT AACATCATCA AGGGAAGAAG CTTGGATCAT TGTCTCAAAAG 1380  
 AGATAT 1386

10

## (2) INFORMATION FOR SEQ ID NO: 30:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741

(B) TYPE: Nucleic acid

15

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

20

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

25

ATGGGGGCTG CGGTGTTTTT CGGCTGCACT TTCGTGCGCT TCGGCCCGGC CTTGCGGCTT 60  
 TTCTTGATCA CTGTGGCTGG GGACCCGCTT CGCGTTATCA TCCTGCTCGC AGGGGCATT 120  
 TTCTGGCTGG TCTCCCTGCT CTTGGCCTCT GTGGTCTGGT TCATCTTGGT CCATGTGACC 180  
 GACCGGCTAG ATGCCCGGCT CCAGTACGGC CTCCTGATT 120  
 30 CTTCTACAGG AGGTGTTCCG CTTTGCCTAC TACAAGCTGC TTAAGAAGGC AGATGAGGGG 300  
 TTAGCATCGC TGAGTGAGGA CGGAAGATCA CCCATCTCCA TCCGCCAGAT GGCCTATGTT 360  
 TCTGGTCTCT CCTTCGGTAT CATCAGTGGT GTCTTCTCTG TTAATCAATAT TTTGGCTGAT 420  
 GCACTTGGGC CAGGTGTGGT TGGGATCCAT GGAGACTCAC CCTATTACTT CCTGACTTCA 480  
 GCCTTTCTGA CAGCAGCCAT TATCCTGCTC CATACCTTTT GGGGAGTTGT GTTCTTTGAT 540  
 35 GCCTGTGAGA GGAGACGGTA CTGGGCTTTG GGCCTGGTGG TTGGGAGTCA CCTACTGACA 600  
 TCGGGACTGA CATTCCTGAA CCCCTGGTAT GAGGCCAGCC TGCTGCCCCAT CTATGCAGTC 660  
 ACTGTTTCCA TGGGGCTCTG GGCCTTCATC ACAGCTGGAG GGTCCCTCCG AAGTATTCAG 720  
 CGCAGCCTCT TGTGTAAGGA C 741



## (2) INFORMATION FOR SEQ ID NO: 31:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10424

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

ATGAACCTCT ATTTACTCCT AGCGAGCAGC ATTCTGTGTG CCTTGATTGT CTTCTGAAA 60  
 TATCGCCGCT TTCAGAGAAA CACTGCGGAA ATGTCATCAA ATTCAACTGC TCTTGCACTA 120  
 GTGAGACCCT CTTCTTCTGG GTTAATTAAC AGCAATACAG ACAACAATCT TGCAGTCTAC 180  
 GACCTCTCTC GGGATATTTT AAATAATTTT CCACACTCAA TAGCCAGGCA GAAGCGAATA 240  
 TTGGTAAACC TCAGTATGGT GGAACAACAG CTGGTTGAAC TGGAACATAC TCTACTTAGC 300  
 AAGGGTTTCA GAGGTGCATC ACCTCACCGG AAATCCACC 339

## (2) INFORMATION FOR SEQ ID NO: 32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Epidermoid carcinoma  
 (C) CELL LINE: KB  
 (D) CLONE NAME: HP10428

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

	ATGGGGAGGT GGGCCCTCGA TGTGGCCTTT TTGTGGAAGG CGGTGTTGAC CCTGGGGCTG	60
	GTGCTTCTCT ACTACTGCTT TCCATCGGC ATCACCTTCT ACAACAAGTG GCTGACAAAG	120
5	AGCTTCCATT TCCCCCTCTT CATGACGATG CTGCACCTGG CCGTGATCTT CCTTCTCTCC	180
	GCCCTGTCCA GGGCGCTGGT TCAGTGCTCC AGCCACAGGG CCCGTGTGGT GCTGAGCTGG	240
	GCGACTACC TCAGAAGAGT GGCTCCACA GCTCTGGCGA CGGCGCTTGA CGTGGGGCTG	300
	TCCAACCTGA GCTTCTGTA TGTACCGTC TCGCTGTACA CAATGACCAA ATCCTCAGCT	360
	GTCTCTTTCA TCTTGATCTT CTCTCTGATC TTCAAGCTGG AGGAGCTGGG GCGGGCACTG	420
10	GTCTCTGGTG TCCTCCTCAT GCGCGGGGGT CTCTTCATGT TCACCTACAA GTCCACACAG	480
	TTCAACGTGG AGGGCTTCGC CTGGTGCTG GGGGCTCGT TCATCGGTGG CATTGCTGG	540
	ACCCTCACC AGATGCTCCT GCAGAAGGCT GAACTCGGCC TCCAGAATCC CATCGACACC	600
	ATGTTCCACC TGCAGCCACT CATGTTCTTG GGGCTCTTCC CTCTCTTTGG TGTATTGAA	660
	GGTCTCCATT TGTCCACATC TGAGAAAATC TTCCGTTTCC AGGACACAGG GCTGCTCCTG	720
15	CGGGTACTTG GGAGCCTCTT CTTGGCGGG ATTCTCGCCT TTGGTTTGGG CTCTCTGAG	780
	TTCTCTCTGG TCTCCAGAAC CTCCAGCCTC ACTCTCTCCA TTGCCGGCAT TTTTAAGGAA	840
	CTCTGCACTT TGCTGTTGGC AGCTCATCTG CTGGGCGATC AGATCAGCCT CCTGAAGTGG	900
	CTGGGCTTCG CCCTCTGCCT CTCGGGAATA TCCCTCCACG TTGCCCTCAA AGCCCTGCAT	960
	TCCAGAGGTG ATGTTGGCCC CAAGGCCTTG AAGGGGCTGG GCTCCAGCCC CGACCTGGAG	1020
20	CTGCTGCTCC GGAGCAGCCA GCGGGAGGAA GGTGACAATG AGGAGGAGGA GTACTTTGTG	1080
	GCCAGGGGC AGCAG	1095

## (2) INFORMATION FOR SEQ ID NO: 33:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## 30 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Stomach cancer
- (D) CLONE NAME: HP10429

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

ATGCCTACCA CAAAGAAGAC ATTGATGTTC TTATCAAGCT TTTTCACCAG CCTTGGGTCC 60  
 TTCATTGTAA TTTGCTCTAT TCTTGGGACA CAAGCATGGA TCACCAGTAC AATTGCTGTT 120  
 AGAGACTCTG CTTCAAATGG GAGCATTTC ATCACTTACG GACTTTTTTCG TGGGGAGAGT 180  
 AGTGAAGAAT TGAGTCACGG ACTTGCAGAA CCAAAGAAAA AGTTTGAGT TTTAGAGATA 240  
 5 CTGAATAATT CTTCCAAAA AACTCTGCAT TCGGTGACTA TCCTGTTCCT GGTCTGAGT 300  
 TTGATCACGT CGCTGCTGAG CTCTGGGTTT ACCTTCTACA ACAGCATCAG CAACCCTTAC 360  
 CAGACATTCC TGGGGCCGAC GGGGGTGTAC ACCTGGAACG GGCTCGGTGC ATCCTTCGTT 420  
 TTTGTGACCA TGATACTGTT TGTGGCGAAC ACGCAGTCCA ACCAACTCTC CGAAGAGTTG 480  
 TTCCAAATGC TTTACCGGC AACCACCAGT AAAGGAACGA CCCACAGTTA CGGATACTCG 540  
 10 TTCTGGCTCA TACTGCTCGT CATTCTTCTA AATATAGTCA CTGTAACCAT CATCATTTTC 600  
 TACCAGAAGG CCAGATACCA GCGGAAGCAG GAGCAGAGAA AGCCAATGGA ATATGCTCCA 660  
 AGGGACGGAA TTTTATTC 678

15 (2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 387

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

30 ATGGCTCGGG GCTCGCTGCG CCGGTTGCTG CGGCTCCTCG TGCTGGGGCT CTGGCTGGCG 60  
 TTGCTGCGCT CCGTGGCCGG GGAGCAAGCG CCAGGCACCG CCCCTGCTC CCGGGGAGC 120  
 TCCTGGAGCG CGGACCTGGA CAAGTGCATG GACTGCGGCT CTGCGAGGC GCGACCGCAC 180  
 AGCGACTTCT GCCTGGGCTG CGCTGCAGCA CCTCTGCCC CCTTCCGGCT GCTTTGGCCC 240  
 35 ATCCTTGGGG GCGCTCTGAG CCTGACCTTC GTGCTGGGGC TGCTTTCTGG CTTTTTGGTC 300  
 TGGAGACGAT GCGCGAGGAG AGAGAAGTTC ACCACCCCA TAGAGGAGAC CGGCGGAGAG 360  
 GGCTGCCAG CTGTGGCGCT GATCCAG 387

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Liver  
 (D) CLONE NAME: HP10433

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCGACGGC TGCTGATCCC TCTGGCCCTG TGGCTGGGCG CGGTGGGCGT GGGCGTCGCC 60  
 GAGCTCACGG AAGCCCAGCG CCGGGGCCCTG CAGGTGGCCC TGGAGGAATT TCACAAGCAC 120  
 CCGCCCGTGC AGTGGGCCTT CCAGGAGACC AGTGTGGAGA GCGCCGTGGA CACGCCCTTC 180  
 CCAGCTGGAA TATTGTGAG GCTGGAATTT AAGCTGCAGC AGACAAGCTG CCGGAAGAGG 240  
 GACTGGAAGA AACCCGAGTG CAAAGTCAGG CCAATGGGA GGAAACGGAA ATGCCTGGCC 300  
 TGCATCAAAC TGGGCTCTGA GGACAAAGTT CTGGGCCGGT TGGTCCACTG CCCCATAGAG 360  
 ACCCAAGTTC TCGGGGAGGC TGAGGAGCAC CAGGAGACCC AGTGCCTCAG GGTGCAGCGG 420  
 GCTGGTGAGG ACCCCCACAG CTTCTACTTC CCTGGACAGT TCGCCTTCTC CAAGGCCCTG 480  
 CCCCGCAGC 489

## (2) INFORMATION FOR SEQ ID NO: 36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10480

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

ATGATCCGCT GCGGCCTGGC CTGCGAGCGC TGCCGCTGGA TCCTGCCCTT GCTCCTACTC      60
AGCGCCCATCG CCTTCGACAT CATCGCGCTG GCCGCGCCGG GCTGGTTGCA GTCTAGCGAC      120
5  CACGGCCAGA CGTCCTCGCT GTGGTGAAA TGCTCCCAAG AGGGCGGCGG CAGCGGGTCC      180
TACGAGGAGG GCTGTCAGAG CCTCATGGAG TACGCGTGGG GTAGAGCAGC GGCTGCCATG      240
CTCTTCTGTG GCTTCATCAT CCTGGTGATC TGTTCATCC TCTCCTTCTT CGCCCTCTGT      300
GGACCCCAAGA TGCTTGCTCTT CCTGAGAGTG ATTGGAGGTC TCCTTGCCCTT GGCTGCTGTG      360
TTCAGATCA TCTCCCTGCT AATTACCCC GTGAAGTACA CCCAGACCTT CACCCTTCAT      420
10 GCCAACCGTG CTGTCACTTA CATCTATAAC TGGCGCTACG GCTTTGGGTG GGCAGCCACG      480
ATTATCTGA TCGGTGTGTC CTCTCTTCTT TGCTGCCTCC CCAACTACGA AGATGACCTT      540
CTGGGCAATG CCAAGCCAG GTACTTCTAC ACATCTGCC      579

```

## 15 (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1502

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Liver

(D) CLONE NAME: HP01263

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

30 (B) EXISTENCE POSITION: 37.. 1185

(C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

```

35 ACAAAGTAC CCATCCTGGG CCTGTCTCTC CACAGA ATG GGT CTG CTC CTT CCC      54
                                     Met Gly Leu Leu Leu Pro
                                     1           5
CTG GCA CTC TGC ATC CTA GTC CTG TGC TGC GGA GCA ATG TCT CCA CCC      102

```

	Leu	Ala	Leu	Cys	Ile	Leu	Val	Leu	Cys	Cys	Gly	Ala	Met	Ser	Pro	Pro	
				10						15					20		
	CAG	CTG	GCC	CTC	AAC	CCC	TCG	GCT	CTG	CTC	TCC	CGG	GGC	TGC	AAT	GAC	150
	Gln	Leu	Ala	Leu	Asn	Pro	Ser	Ala	Leu	Leu	Ser	Arg	Gly	Cys	Asn	Asp	
5				25						30					35		
	TCC	GAT	GTG	CTG	GCA	GTT	GCA	GGC	TTT	GCC	CTG	CGG	GAT	ATT	AAC	AAA	198
	Ser	Asp	Val	Leu	Ala	Val	Ala	Gly	Phe	Ala	Leu	Arg	Asp	Ile	Asn	Lys	
				40						45					50		
	GAC	AGA	AAG	GAT	GGC	TAT	GTG	CTG	AGA	CTC	AAC	CGA	GTG	AAC	GAC	GCC	246
10	Asp	Arg	Lys	Asp	Gly	Tyr	Val	Leu	Arg	Leu	Asn	Arg	Val	Asn	Asp	Ala	
				55						60					65	70	
	CAG	GAA	TAC	AGA	CGG	GGT	GGC	CTG	GGA	TCT	CTG	TTC	TAT	CTT	ACA	CTG	294
	Gln	Glu	Tyr	Arg	Arg	Gly	Gly	Leu	Gly	Ser	Leu	Phe	Tyr	Leu	Thr	Leu	
										75					80	85	
15	GAT	GTG	CTA	GAG	ACT	GAC	TGC	CAT	GTG	CTC	AGA	AAG	AAG	GCA	TGG	CAA	342
	Asp	Val	Leu	Glu	Thr	Asp	Cys	His	Val	Leu	Arg	Lys	Lys	Ala	Trp	Gln	
										90					95	100	
	GAC	TGT	GGA	ATG	AGG	ATA	TTT	TTT	GAA	TCA	GTT	TAT	GGT	CAA	TGC	AAA	390
	Asp	Cys	Gly	Met	Arg	Ile	Phe	Phe	Glu	Ser	Val	Tyr	Gly	Gln	Cys	Lys	
20				105						110					115		
	GCA	ATA	TTT	TAT	ATG	AAC	AAC	CCA	AGT	AGA	GTT	CTC	TAT	TTA	GCT	GCT	438
	Ala	Ile	Phe	Tyr	Met	Asn	Asn	Pro	Ser	Arg	Val	Leu	Tyr	Leu	Ala	Ala	
										120					125	130	
	TAT	AAC	TGT	ACT	CTT	CGC	CCA	GTT	TCA	AAA	AAA	AAG	ATT	TAC	ATG	ACG	486
25	Tyr	Asn	Cys	Thr	Leu	Arg	Pro	Val	Ser	Lys	Lys	Lys	Ile	Tyr	Met	Thr	
										135					140	145	150
	TGC	CCT	GAC	TGC	CCA	AGC	TCC	ATA	CCC	ACT	GAC	TCT	TCC	AAT	CAC	CAA	534
	Cys	Pro	Asp	Cys	Pro	Ser	Ser	Ile	Pro	Thr	Asp	Ser	Ser	Asn	His	Gln	
										155					160	165	
30	GTG	CTG	GAG	GCT	GCC	ACC	GAG	TCT	CTT	GCG	AAA	TAC	AAC	AAT	GAG	AAC	582
	Val	Leu	Glu	Ala	Ala	Thr	Glu	Ser	Leu	Ala	Lys	Tyr	Asn	Asn	Glu	Asn	
										170					175	180	
	ACA	TCC	AAG	CAG	TAT	TCT	CTC	TTC	AAA	GTC	ACC	AGG	GCT	TCT	AGC	CAG	630
	Thr	Ser	Lys	Gln	Tyr	Ser	Leu	Phe	Lys	Val	Thr	Arg	Ala	Ser	Ser	Gln	
35				185						190					195		
	TGG	GTG	GTC	GGC	CCT	TCT	TAC	TTT	GTG	GAA	TAC	TTA	ATT	AAA	GAA	TCA	678
	Trp	Val	Val	Gly	Pro	Ser	Tyr	Phe	Val	Glu	Tyr	Leu	Ile	Lys	Glu	Ser	
				200						205					210		

	CCA TGT ACT AAA TCC CAG GCC AGC AGC TGT TCA CTT CAG TCC TCC GAC	726
	Pro Cys Thr Lys Ser Gln Ala Ser Ser Cys Ser Leu Gln Ser Ser Asp	
	215 220 225 230	
	TCT GTG CCT GTT GGT CTT TGC AAA GGT TCT CTG ACT CGA ACA CAC TGG	774
5	Ser Val Pro Val Gly Leu Cys Lys Gly Ser Leu Thr Arg Thr His Trp	
	235 240 245	
	GAA AAG TTT GTC TCT GTG ACT TGT GAC TTC TTT GAA TCA CAG GCT CCA	822
	Glu Lys Phe Val Ser Val Thr Cys Asp Phe Phe Glu Ser Gln Ala Pro	
	250 255 260	
10	GCC ACT GGA AGT GAA AAC TCT GCT GTT AAC CAG AAA CCT ACA AAC CTT	870
	Ala Thr Gly Ser Glu Asn Ser Ala Val Asn Gln Lys Pro Thr Asn Leu	
	265 270 275	
	CCC AAG GTG GAA GAA TCC CAG CAG AAA AAC ACC CCC CCA ACA GAC TCC	918
	Pro Lys Val Glu Glu Ser Gln Gln Lys Asn Thr Pro Pro Thr Asp Ser	
15	280 285 290	
	CCC TCC AAA GCT GGG CCA AGA GGA TCT GTC CAA TAT CTT CCT GAC TTG	966
	Pro Ser Lys Ala Gly Pro Arg Gly Ser Val Gln Tyr Leu Pro Asp Leu	
	295 300 305 310	
	GAT GAT AAA AAT TCC CAG GAA AAG GGC CCT CAG GAG GCC TTT CCT GTG	1014
20	Asp Asp Lys Asn Ser Gln Glu Lys Gly Pro Gln Glu Ala Phe Pro Val	
	315 320 325	
	CAT CTG GAC CTA ACC ACG AAT CCC CAG GGA GAA ACC CTG GAT ATT TCC	1062
	His Leu Asp Leu Thr Thr Asn Pro Gln Gly Glu Thr Leu Asp Ile Ser	
	330 335 340	
25	TTC CTC TTC CTG GAG CCT ATG GAG GAG AAG CTG GTT GTC CTG CCT TTC	1110
	Phe Leu Phe Leu Glu Pro Met Glu Glu Lys Leu Val Val Leu Pro Phe	
	345 350 355	
	CCC AAA GAA AAA GCA CGC ACT GCT GAG TGC CCA GGG CCA GCC CAG AAT	1158
	Pro Lys Glu Lys Ala Arg Thr Ala Glu Cys Pro Gly Pro Ala Gln Asn	
30	360 365 370	
	GCC AGC CCT CTT GTC CTT CCG CCA TGAGAATCAC ACAGAGTCTT CTGTAGGG	1210
	Ala Ser Pro Leu Val Leu Pro Pro	
	375 380	
	GTATGGTGGC CCGCATGACA TGGGAGGCGA TGGGGACGAT GGACAGAGAC AGAGCGTGCA	1270
35	CACGTAGAGT GGCTAGTGAA GGACGCCCTTT TTGACTCTTC TTGCTCTCAG CATGTTGACT	1330
	GGGATTGGAA ATAATGAGAC TGAGCCCTCG GCTTGGGCTG CACTCTACCC TGTACACTGC	1390
	CTTGTAACCT GAGCTGCATC ACCTCCTAAA CTGAGCAGTC TCATACCATG GAGAGATGCC	1450
	TCTCTTATGT CTTAGCCAC TCACCTATAA AGATACTTAT CTTTTCAGCA GT	1502

## (2) INFORMATION FOR SEQ ID NO: 38:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1349

5 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## 10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Liver

(D) CLONE NAME: HP01299

15

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 111.. 1064

(C) CHARACTERIZATION METHOD: E

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

```

AGCAGTTGGG GCAGGAGGAA GCCGACTGCT GCCTGGTCTG CAAAGAAGTC CTTTCAAGTC      60
TCTAGGACTG GACTCTTCCT AAGCAAGTCC GAGAAGGAAG CACCCTCACT ATG TGG      116
25                                     Met Trp
                                     1
CTC TAC CTG GCG GCC TTC GTG GGC CTG TAC TAC CTT CTG CAC TGG TAC
164
Leu Tyr Leu Ala Ala Phe Val Gly Leu Tyr Tyr Leu Leu His Trp Tyr
30           5           10           15
CGG GAG AGG CAG GTG GTG AGC CAC CTC CAA GAC AAG TAT GTC TTT ATC      212
Arg Glu Arg Gln Val Val Ser His Leu Gln Asp Lys Tyr Val Phe Ile
           20           25           30
ACG GGC TGT GAC TCG GGC TTT GGG AAC CTG CTG GCC AGA CAG CTG GAT      260
35 Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Leu Ala Arg Gln Leu Asp
           35           40           45           50
GCA CGA GGC TTG AGA GTG CTG GCT GCG TGT CTG ACG GAG AAG GGG GCC      308
Ala Arg Gly Leu Arg Val Leu Ala Ala Cys Leu Thr Glu Lys Gly Ala

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		55		60		65		
	GAG CAG CTG AGG GGC CAG ACG TCT GAC AGG CTG GAG ACG GTG ACC CTG							356
	Glu Gln Leu Arg Gly Gln Thr Ser Asp Arg Leu Glu Thr Val Thr Leu							
	70		75		80			
5	GAT GTT ACC AAG ATG GAG AGC ATC GCT GCA GCT ACT CAG TGG GTG AAG							404
	Asp Val Thr Lys Met Glu Ser Ile Ala Ala Ala Thr Gln Trp Val Lys							
	85		90		95			
	GAG CAT GTG GGG GAC AGA GGA CTC TGG GGA CTG GTG AAC AAT GCA GGC							452
	Glu His Val Gly Asp Arg Gly Leu Trp Gly Leu Val Asn Asn Ala Gly							
10	100		105		110			
	ATT CTT ACA CCA ATT ACC TTA TGT GAG TGG CTG AAC ACT GAG GAC TCT							500
	Ile Leu Thr Pro Ile Thr Leu Cys Glu Trp Leu Asn Thr Glu Asp Ser							
	115		120		125		130	
	ATG AAT ATG CTC AAA GTG AAC CTC ATT GGT GTG ATC CAG GTG ACC TTG							548
15	Met Asn Met Leu Lys Val Asn Leu Ile Gly Val Ile Gln Val Thr Leu							
	135		140		145			
	AGC ATG CTT CCT TTG GTG AGG AGA GCA CGG GGA AGA ATT GTC AAT GTC							596
	Ser Met Leu Pro Leu Val Arg Arg Ala Arg Gly Arg Ile Val Asn Val							
	150		155		160			
20	TCC AGC ATT CTG GGA AGA GTT GCT TTC TTT GTA GGA GGC TAC TGT GTC							644
	Ser Ser Ile Leu Gly Arg Val Ala Phe Phe Val Gly Gly Tyr Cys Val							
	165		170		175			
	TCC AAG TAT GGA GTG GAA GCC TTT TCA GAT ATT CTG AGG CGT GAG ATT							692
	Ser Lys Tyr Gly Val Glu Ala Phe Ser Asp Ile Leu Arg Arg Glu Ile							
25	180		185		190			
	CAA CAT TTT GGG GTG AAA ATC AGC ATA GTT GAA CCT GGC TAC TTC AGA							740
	Gln His Phe Gly Val Lys Ile Ser Ile Val Glu Pro Gly Tyr Phe Arg							
	195		200		205		210	
	ACG GGA ATG ACA AAC ATG ACA CAG TCC TTA GAG CGA ATG AAG CAA AGT							788
30	Thr Gly Met Thr Asn Met Thr Gln Ser Leu Glu Arg Met Lys Gln Ser							
	215		220		225			
	TGG AAA GAA GCC CCC AAG CAT ATT AAG GAG ACC TAT GGA CAG CAG TAT							836
	Trp Lys Glu Ala Pro Lys His Ile Lys Glu Thr Tyr Gly Gln Gln Tyr							
	230		235		240			
35	TTT GAT GCC CTT TAC AAT ATC ATG AAG GAA GGG CTG TTG AAT TGT AGC							884
	Phe Asp Ala Leu Tyr Asn Ile Met Lys Glu Gly Leu Leu Asn Cys Ser							
	245		250		255			
	ACA AAC CTG AAC CTG GTC ACT GAC TGC ATG GAA CAT GCT CTG ACA TCG							932

	Thr	Asn	Leu	Asn	Leu	Val	Thr	Asp	Cys	Met	Glu	His	Ala	Leu	Thr	Ser	
	260						265						270				
	GTG	CAT	CCG	CGA	ACT	CGA	TAT	TCA	GCT	GGC	TGG	GAT	GCT	AAA	TTT	TTC	980
	Val	His	Pro	Arg	Thr	Arg	Tyr	Ser	Ala	Gly	Trp	Asp	Ala	Lys	Phe	Phe	
5	275						280						285				290
	TTC	ATC	CCT	CTA	TCT	TAT	TTA	CCT	ACA	TCA	CTG	GCA	GAC	TAC	ATT	TTG	1028
	Phe	Ile	Pro	Leu	Ser	Tyr	Leu	Pro	Thr	Ser	Leu	Ala	Asp	Tyr	Ile	Leu	
							295						300				305
	ACT	AGA	TCT	TGG	CCC	AAA	CCA	GCC	CAG	GCA	GTC	TAAAGAAAAC	TGGGTTGGT				1080
10	Thr	Arg	Ser	Trp	Pro	Lys	Pro	Ala	Gln	Ala	Val						
							310						315				
	GCTTCTTGG	ATGAAGGCAA	AAATCTGAAA	TTGTTAGTGT	CTCAGTAATC	CTGATTTAGA											1140
	ACCCAGGCTT	TTTGTAACAA	TGTGTTTTCT	TGCCTAAATT	CATTTATCTG	GCATCATCAG											1200
	AGTACTAACA	TGTTTATATT	TCAGATATCC	AAAGCTTACC	ACTTTAGGTG	ATGAATCTTT											1260
15	ACTATTTTAG	CCCTTTTTTG	ATGAGACTAT	TTGTCTAAAG	TGAATCATT	GTTCTTGCCT											1320
	TATTAAACAG	AGTAGATGGA	AAACAATT														1349

## (2) INFORMATION FOR SEQ ID NO: 39:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1643
  - (B) TYPE: Nucleic acid
  - (C) STRANDEDNESS: Double
  - (D) TOPOLOGY: Linear
- 25 (ii) SEQUENCE KIND: cDNA to mRNA
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Homo sapiens*
  - (B) CELL KIND: Liver
  - (D) CLONE NAME: HP01347
- 30 (ix) SEQUENCE CHARACTERISTICS:
- (A) CHARACTERIZATION CODE: CDS
  - (B) EXISTENCE POSITION: 25.. 915
  - (C) CHARACTERIZATION METHOD: E
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

	AACATCTGGG GACAGCGGGA AAAC ATG AGT GAC TCC AAG GAA CCA AGG GTG	51
	Met Ser Asp Ser Lys Glu Pro Arg Val	
	1 5	
	CAG CAG CTG GGC CTC CTG GGG TGT CTT GGC CAT GGC GCC CTG GTG CTG	99
5	Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu	
	10 15 20 25	
	CAA CTC CTC TCC TTC ATG CTC TTG GCT GGG GTC CTG GTG GCC ATC CTT	147
	Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu	
	30 35 40	
10	GTC CAA GTG TCC AAG GTC CCC AGC TCC CTA AGT CAG GAA CAA TCC GAG	195
	Val Gln Val Ser Lys Val Pro Ser Ser Leu Ser Gln Glu Gln Ser Glu	
	45 50 55	
	CAA GAC GCA ATC TAC CAG AAC CTG ACC CAG CTT AAA GCT GCA GTG GGT	243
	Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly	
15	60 65 70	
	GAG CTC TCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC	291
	Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr	
	75 80 85	
	CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG	339
20	Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
	90 95 100 105	
	GAG ATC TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG	387
	Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu	
	110 115 120	
25	CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACC CGG CTG	435
	Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu	
	125 130 135	
	AAG GCT GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC	483
	Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile	
30	140 145 150	
	TAC CAG GAG CTG ACC CGG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAG	531
	Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
	155 160 165	
	AAA TCC AAG CTG CAG GAG ATC TAC CAG GAG CTG ACG GAG CTG AAG GCT	579
35	Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Glu Leu Lys Ala	
	170 175 180 185	
	GCA GTG GGT GAG TTG CCA GAG AAA TCC AAG CTG CAG GAG ATC TAC CAG	627
	Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln	

	190	195	200	
	GAG CTG ACC CAG CTG AAG GCT GCA GTG GGT GAG TTG CCA GAC CAG TCC			675
	Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Asp Gln Ser			
	205	210	215	
5	AAG CAG CAG CAA ATC TAT CAA GAA CTG ACC GAT TTG AAG ACT GCA TTT			723
	Lys Gln Gln Gln Ile Tyr Gln Glu Leu Thr Asp Leu Lys Thr Ala Phe			
	220	225	230	
	GAA CGC CTG TGC CGC CAC TGT CCC AAG GAC TGG ACA TTC TTC CAA GGA			771
	Glu Arg Leu Cys Arg His Cys Pro Lys Asp Trp Thr Phe Phe Gln Gly			
10	235	240	245	
	AAC TGT TAC TTC ATG TCT AAC TCC CAG CGG AAC TGG CAC GAC TCC GTC			819
	Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Val			
	250	255	260	265
	ACC GCC TGC CAG GAA GTG AGG GCC CAG CTC GTC GTA ATC AAA ACT GCT			867
15	Thr Ala Cys Gln Glu Val Arg Ala Gln Leu Val Val Ile Lys Thr Ala			
	270	275	280	
	GAG GAG CAG CTT CCA GCG GTA CTG GAA CAG TGG AGA ACC CAA CAA			912
	Glu Glu Gln Leu Pro Ala Val Leu Glu Gln Trp Arg Thr Gln Gln			
	285	290	295	
20	TAGCGGGAAT GAAGACTGTG CGGAATTTAG TGGCAGTGGC TGGACGACA ATCGATGT			970
	GACGTTGACA ATTACTGGAT CTGCAAAAAG CCCGCAGCCT GCTTCAGAGA CGAATAGTTG			1030
	TTTCCTGCT AGCCTCAGCC TCCATTGTGG TATAGCAGAA CTTCACCCAC TTGTAAGCCA			1090
	GCGCTTCTTC TCTCCATCCT TGGACCTTCA CAAATGCCCT GAGACGGTTC TCTGTTGAT			1150
	TTTTCATCCC CTATGAACCT GGGTCTTATT CTGTCCTTCT GATGCCTCCA AGTTTCCCTG			1210
25	GTGTAGAGCT TGTGTTCTTG GCCCATCCTT GGAGCTTTAT AAGTGACCTG AGTGGGATGC			1270
	ATTTAGGGGG CGGGCTTGGT ATGTTGTATG AATCCACTCT CTGTTCTTTT TGGAGATTAG			1330
	ACTATTTGGA TTCATGTGTA GCTGCCCTGT CCCCTGGGGC TTTATCTCAT CCATGCAAAAC			1390
	TACCATCTGC TCAACTTCCA GCTACACCCC GTGCACCCTT TTGACTGGGG ACTTGCTGGT			1450
	TGAAGGAGCT CATCTTGAG GCTGGAAGCA CCAGGAATT AATCCCCCA GTCAACCAAT			1510
30	GGCATCCAGA GAGGGCATGG AGGCTCCATA CAACCTCTTC CACCCCCACA TCTTTCCTTG			1570
	TCCTATACAT GTCTTCCATT TGGCTGTTTC TGAGTTGTAG CCTTTATAAT AAAGTGGTAA			1630
	ATGTTGTAAC TGC			1643

## 35 (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01440

10 (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 38.. 631

(C) CHARACTERIZATION METHOD: E

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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ACTTTCACCTC ACCGCCTGTC CTCCTGACA CCTCACC ATG TGT ACG GGA AAA TGT      55
                                     Met Cys Thr Gly Lys Cys
                                     1           5
20 GCC CGC TGT GTG GGG CTC TCC CTC ATT ACC CTC TGC CTC GTC TGC ATT      103
   Ala Arg Cys Val Gly Leu Ser Leu Ile Thr Leu Cys Leu Val Cys Ile
       10           15           20
   GTG GCC AAC GCC CTC CTG CTG GTA CCT AAT GGG GAG ACC TCC TGG ACC      151
   Val Ala Asn Ala Leu Leu Leu Val Pro Asn Gly Glu Thr Ser Trp Thr
25   AAC ACC AAC CAT CTC AGC TTG CAA GTC TGG CTC ATG GGC GGC TTC ATT      199
   Asn Thr Asn His Leu Ser Leu Gln Val Trp Leu Met Gly Gly Phe Ile
       40           45           50
   GGC GGC GGC CTA ATG GTA CTG TGT CCG GGG ATT GCA GCC GTT CGG GCA      247
30 Gly Gly Gly Leu Met Val Leu Cys Pro Gly Ile Ala Ala Val Arg Ala
   55           60           65           70
   GGG GGC AAG GGC TGC TGT GGT GCT GGG TGC TGT GGA AAC CGC TGC AGG      295
   Gly Gly Lys Gly Cys Cys Gly Ala Gly Cys Cys Gly Asn Arg Cys Arg
       75           80           85
35 ATG CTG CGC TCG GTC TTC TCC TCG GCG TTC GGG GTG CTT GGT GCC ATC      343
   Met Leu Arg Ser Val Phe Ser Ser Ala Phe Gly Val Leu Gly Ala Ile
       90           95           100
   TAC TGC CTC TCG GTG TCT GGA GCT GGG CTC CGA AAT GGA CCC AGA TGC      391

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	Tyr	Cys	Leu	Ser	Val	Ser	Gly	Ala	Gly	Leu	Arg	Asn	Gly	Pro	Arg	Cys	
	TTA	ATG	AAC	GGC	GAG	TGG	GGC	TAC	CAC	TTC	GAA	GAC	ACC	GCG	GGA	GCT	439
	Leu	Met	Asn	Gly	Glu	Trp	Gly	Tyr	His	Phe	Glu	Asp	Thr	Ala	Gly	Ala	
5																	
	TAC	TTG	CTC	AAC	CGC	ACT	CTA	TGG	GAT	CGG	TGC	GAG	GCG	CCC	CCT	CGC	487
	Tyr	Leu	Leu	Asn	Arg	Thr	Leu	Trp	Asp	Arg	Cys	Glu	Ala	Pro	Pro	Arg	
	GTG	GTC	CCC	TGG	AAT	GTG	ACG	CTC	TTC	TCG	CTG	CTG	GTG	GCC	GCC	TCC	535
10	Val	Val	Pro	Trp	Asn	Val	Thr	Leu	Phe	Ser	Leu	Leu	Val	Ala	Ala	Ser	
	TGC	CTG	GAG	ATA	GTA	CTG	TGT	GGG	ATC	CAG	CTG	GTG	AAC	GCG	ACC	ATT	583
	Cys	Leu	Glu	Ile	Val	Leu	Cys	Gly	Ile	Gln	Leu	Val	Asn	Ala	Thr	Ile	
15	GGT	GTC	TTC	TGC	GGC	GAT	TGC	AGG	AAA	AAA	CAG	GAC	ACC	CCT	CAC	TG	630
	Gly	Val	Phe	Cys	Gly	Asp	Cys	Arg	Lys	Gln	Asp	Thr	Pro	His			
	AGGCTCCACT	GACCGCCGGG	TTACACCTGC	TCCTTCCTGG	ACGCCTACCT	GGCTCGCTCA											690
	CTCCCTTGCT	CGCTAGAATA	AACTGCTTTG	CGCTCTCTT													729

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1322

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP01526

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 84.. 749

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

	GAGCGGCAGG TCTGGGCTGC AGTAGGTCCC GGCAACCGCA GGCTCGGGGC GGGCGCTGGG	60
	CGCGGGATCC GACTCTAGTC GTA ATG GAG GCG GGC GGC TTT CTG GAC TCG CTC	113
5	Met Glu Ala Gly Gly Phe Leu Asp Ser Leu	
	1 5 10	
	ATT TAC GGA GCA TGC GTG GTC TTC ACC CTT GGC ATG TTC TCC GCC GGC	161
	Ile Tyr Gly Ala Cys Val Val Phe Thr Leu Gly Met Phe Ser Ala Gly	
	15 20 25	
10	CTC TCG GAC CTC AGG CAC ATG CGA ATG ACC CGG AGT GTG GAC AAC GTC	209
	Leu Ser Asp Leu Arg His Met Arg Met Thr Arg Ser Val Asp Asn Val	
	30 35 40	
	CAG TTC CTG CCC TTT CTC ACC ACG GAA GTC AAC AAC CTG GGC TGG CTG	257
	Gln Phe Leu Pro Phe Leu Thr Thr Glu Val Asn Asn Leu Gly Trp Leu	
15	45 50 55	
	AGT TAT GGG GCT TTG AAG GGA GAC GGG ATC CTC ATC GTC GTC AAC ACA	305
	Ser Tyr Gly Ala Leu Lys Gly Asp Gly Ile Leu Ile Val Val Asn Thr	
	60 65 70	
	GTG GGT GCT GCG CTT CAG ACC CTG TAT ATC TTG GCA TAT CTG CAT TAC	353
20	Val Gly Ala Ala Leu Gln Thr Leu Tyr Ile Leu Ala Tyr Leu His Tyr	
	75 80 85 90	
	TGC CCT CGG AAG CGT GTT GTG CTC CTA CAG ACT GCA ACC CTG CTA GGG	401
	Cys Pro Arg Lys Arg Val Val Leu Leu Gln Thr Ala Thr Leu Leu Gly	
	95 100 105	
25	CTC CTT CTC CTG GGT TAT GGC TAC TTT TGG CTC CTG GTA CCC AAC CCT	449
	Val Leu Leu Leu Gly Tyr Gly Tyr Phe Trp Leu Leu Val Pro Asn Pro	
	110 115 120	
	GAG GCC CGG CTT CAG CAG TTG GGC CTC TTC TGC AGT GTC TTC ACC ATC	497
	Glu Ala Arg Leu Gln Gln Leu Gly Leu Phe Cys Ser Val Phe Thr Ile	
30	125 130 135	
	AGC ATG TAC CTC TCA CCA CTG GCT GAC TTG GCT AAG GTG ATT CAA ACT	545
	Ser Met Tyr Leu Ser Pro Leu Ala Asp Leu Ala Lys Val Ile Gln Thr	
	140 145 150	
	AAA TCA ACC CAA TGT CTC TCC TAC CCA CTC ACC ATT GCT ACC CTT CTC	593
35	Lys Ser Thr Gln Cys Leu Ser Tyr Pro Leu Thr Ile Ala Thr Leu Leu	
	155 160 165 170	
	ACC TCT GCC TCC TGG TGC CTC TAT GGG TTT CGA CTC AGA GAT CCC TAT	641
	Thr Ser Ala Ser Trp Cys Leu Tyr Gly Phe Arg Leu Arg Asp Pro Tyr	

	175	180	185	
	ATC ATG GTG TCC AAC TTT CCA GGA ATC GTC ACC AGC TTT ATC CGC TTC			689
	Ile Met Val Ser Asn Phe Pro Gly Ile Val Thr Ser Phe Ile Arg Phe			
	190	195	200	
5	TGG CTT TTC TGG AAG TAC CCC CAG GAG CAA GAC AGG AAC TAC TGG CTC			737
	Trp Leu Phe Trp Lys Tyr Pro Gln Glu Gln Asp Arg Asn Tyr Trp Leu			
	205	210	215	
	CTG CAA ACC TGAGGCTGCT CATCTGACCA CTGGGCACCT TAGTGCCAAC CTGA			790
	Leu Gln Thr			
10	220			
	ACCAAAGAGA CCTCCTTGTT TCAGCTGGGC CTGCTGTCCA GCTTCCCAGG TGCAGTGGGT			850
	TGTGGGAACA AGAGTAGACT TTGAGGATAA AAGGACCAAA GAAAAAGCTT TACTTAGATG			910
	ATTGATTGGG GCCTAGGAGA TGAATCACT TTTTATTTT TAGAGATTTT TTTTTTAAT			970
	TTTGGAGGTT GGGGTGCAAT CTTTAGAATA TGCCTTAAAA GGCCGGGCGC GGTGGCTCAC			1030
15	GCCTGTAATC CCAGCACTTT GGGAGGCCAA GGTGGCGGA TCGCCTGAGG TCAGGAGTTC			1090
	AAGACCAACC TGACTAACAT GGTGAAACCC CATCTCTACT AAAAAACAA AATTAGCCAG			1150
	GCATGATGGC ACATGCCTGT AATCCCAGAT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT			1210
	GAACCCAGGA GGTGGAGGTT GCAGTGAGCT GAGATCGTGC CATTGTGATA TGAATATGCC			1270
	TTATATGCTG ATATGAATAT GCCTTAAAT AAAGTGTTC CCACCCCTGC CC			1322

## (2) INFORMATION FOR SEQ ID NO: 42:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3045

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10230

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 191.. 946

(C) CHARACTERIZATION METHOD: E



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GTTTCGCCTC AGAAGGCTGC CTCGCTGGTC CGAATTCGGT GCGGCCACGT CCGCCCGTCT 60  
 CCGCCTTCTG CATCGGGGCT TCGGCGGCTT CCACCTAGAC ACCTAACAGT CCGCGAGCCG 120  
 5 GCGCGCTCGT GAGGGGGTGC GCACGGGGAG TCGGGCGGTC TTGTGCATCT TGGCTACCTG 180  
 TGGGTCAAG ATG TCG GAC ATC GGA GAC TGG TTC AGG AGC ATC CCG GCG 229  
 Met Ser Asp Ile Gly Asp Trp Phe Arg Ser Ile Pro Ala  
 1 5 10  
 ATC ACG CGC TAT TGG TTC GCC GCC ACC GTC GCC GTG CCC TTG GTC GGC 277  
 10 Ile Thr Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly  
 15 20 25  
 AAA CTC GGC CTC ATC AGC CCG GCC TAC CTC TTC CTC TGG CCC GAA GCC 325  
 Lys Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala  
 30 35 40 45  
 15 TTC CTT TAT CGC TTT CAG ATT TGG AGG CCA ATC ACT GCC ACC TTT TAT 373  
 Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe Tyr  
 50 55 60  
 TTC CCT GTG GGT CCA GGA ACT GGA TTT CTT TAT TTG GTC AAT TTA TAT 421  
 Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn Leu Tyr  
 20 65 70 75  
 TTC TTA TAT CAG TAT TCT ACG CGA CTT GAA ACA GGA GCT TTT GAT GGG 469  
 Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala Phe Asp Gly  
 80 85 90  
 AGG CCA GCA GAC TAT TTA TTC ATG CTC CTC TTT AAC TGG ATT TGC ATC 517  
 25 Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn Trp Ile Cys Ile  
 95 100 105  
 GTG ATT ACT GGC TTA GCA ATG GAT ATG CAG TTG CTG ATG ATT CCT CTG 565  
 Val Ile Thr Gly Leu Ala Met Asp Met Gln Leu Met Ile Pro Leu  
 110 115 120 125  
 30 ATC ATG TCA GTA CTT TAT GTC TGG GCC CAG CTG AAC AGA GAC ATG ATT 613  
 Ile Met Ser Val Leu Tyr Val Trp Ala Gln Leu Asn Arg Asp Met Ile  
 130 135 140  
 GTA TCA TTT TGG TTT GGA ACA CGA TTT AAG GCC TGC TAT TTA CCC TGG 661  
 Val Ser Phe Trp Phe Gly Thr Arg Phe Lys Ala Cys Tyr Leu Pro Trp  
 35 145 150 155  
 GTT ATC CTT GGA TTC AAC TAT ATC ATC GGA GGC TCG GTA ATC AAT GAG 709  
 Val Ile Leu Gly Phe Asn Tyr Ile Ile Gly Gly Ser Val Ile Asn Glu  
 160 165 170

	CTT ATT GGA AAT CTG GTT GGA CAT CTT TAT TTT TTC CTA ATG TTC AGA	757
	Leu Ile Gly Asn Leu Val Gly His Leu Tyr Phe Phe Leu Met Phe Arg	
	175 180 185	
	TAC CCA ATG GAC TTG GGA GGA AGA AAT TTT CTA TCC ACA CCT CAG TTT	805
5	Tyr Pro Met Asp Leu Gly Gly Arg Asn Phe Leu Ser Thr Pro Gln Phe	
	190 195 200 205	
	TTG TAC CGC TGG CTG CCC AGT AGG AGA GGA GGA GTA TCA GGA TTT GGT	853
	Leu Tyr Arg Trp Leu Pro Ser Arg Arg Gly Gly Val Ser Gly Phe Gly	
	210 215 220	
10	GTG CCC CCT GCT AGC ATG AGG CGA GCT GCT GAT CAG AAT GGC GGA GGC	901
	Val Pro Pro Ala Ser Met Arg Arg Ala Ala Asp Gln Asn Gly Gly Gly	
	225 230 235	
	GGG AGA CAC AAC TGG GGC CAG GGC TTT CGA CTT GGA GAC CAG TGAAGGG	950
	Gly Arg His Asn Trp Gly Gln Gly Phe Arg Leu Gly Asp Gln	
15	240 245 250	
	GCGGCCTCGG GCAGCCGCTC CTCTCAAGCC ACATTTCCTC CCAGTGCTGG GTGCGCTTAA	1010
	CAACTGCGTT CTGGCTAACA CTGTTGGACC TGACCCACAC TGAATGTAGT CTTTCAGTAC	1070
	GAGACAAAGT TTCTTAAATC CCGAAGAAAA ATATAAGTGT TCCACAAGTT TCACGATTCT	1130
	CATTCAAGTC CTTACTGCTG TGAAGAACAA ATACCAACTG TGCAAATTGC AAAACTGACT	1190
20	ACATTTTTTG GTGCTCTCTC TTCTCCCTT TCCGTCTGAA TAATGGGTTT TAGCGGGTCC	1250
	TAGTCTGCTG GCATTGAGCT GGGGCTGGGT CACCAAAACC TTCCCAAAAG GACCCCTATC	1310
	TCCTTCTTGC ACACATGCCT CTCTCCCACT TTTCCCAACC CCCACATTTG CAACTAGAAG	1370
	AGGTTGCCCA TAAAATTGCT CTGCCCTTGA CAGGTTCTGT TATTTATTGA CTTTGGCCAA	1430
	GGCTTGGTCA CAACAATCAT ATTCACGTAA TTTTCCCTT TTGGTGCGAG AACTGTAGCA	1490
25	ATAGGGGGAG AAGACAAGCA GCGGATGAAG CGTTTTCTCA GCTTTTGGAA TTGCTTCGAC	1550
	CTGACATCCG TTGTAACCGT TTGCCACTTC TTCAGATATT TTTATAAAAA AGTACCACTG	1610
	AGTCAGTCAG GGCCACAGAT TGGTATTAAT GAGATACGAG GGTGTGTGCT GGGTGTGTTG	1670
	TTCTGAGCT AAGTGATCAA GACTGTAGTG GAGTTGCAGC TAACATGGGT TAGGTTTAAA	1730
	CCGTGGGGGA TGCAACCCCT TTGCGTTTCA TATGTAGGCC TACTGGCTTT GTGTAGCTGG	1790
30	AGTAGTTGGG TTGCTTTGTG TTAGGAGGAT CCAGATCATG TTGGCTACAG GGAGATGCTC	1850
	TCCTTGAGAG GCTCCTGGGC ATTGATTCCA TTTCAATCTC ATTCTGGATA TGTGTTTCATT	1910
	GAGTAAAGGA GGAGAGACCC TCATACGCTA TTTAAATGTC ACTTTTTTGC CTATCCCCCG	1970
	TTTTTTGGTC ATGTTTCAAT TAATTGTGAG GAAGGCGCAG CTCCTCTCTG CACGTAGATC	2030
	ATTTTTTAAA GCTAATGTAA GCACATCTAA GGAATAACA TGATTTAAGG TTGAAATGGC	2090
35	TTTGAATCA TTTGGGTTTG AGGGTGTGTT ATTTTGAGTC ATGAATGTAC AAGCTCTGTG	2150
	AATCAGACCA GCTTAAATAC CCACACCTTT TTTTCGTAGG TGGGCTTTTC CTATCAGAGC	2210
	TTGGCTCATA ACCAAATAAA GTTTTTTGAA GGCCATGGCT TTTACACAGC TTATTTTATT	2270
	TTATGACGTT ATCTGAAAGC AGACTGTTAG GAGCAGTATT GAGTGGCTGT CACACTTTGA	2330

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GGCAACTAAA AAGGCTTCAA ACGTTTGGAT CAGTTTCTTT TCAGGAAACA TTGTGCTCTA 2390
ACAGTATGAC TATTCTTTCC CCCACTCTTA AACAGTGTGA TGTGTGTTAT CCTAGGAAAT 2450
GAGAGTTGGC AAACAACCTC TCATTTTGAA TAGAGTTTGT GTGTACCTCT CCATATTTAA 2510
TTTATATGAT AAAATAGGTG GGGAGAGTCT GAACCTTAAC TGTCATGTTT TGTGTTTCAT 2570
5 CTGTGGCCAC AATAAAGTTT ACTTGTAATA TTTTAGAGGC CATTACTCCA ATTATGTTGC 2630
ACGTACACTC ATTGTACAGG CGTGAGACT CATTGTATGT ATAAGAATAT TCTGACAGTG 2690
AGTGACCCGG AGTCTCTGGT GTACCTCTT ACCAGTCAGC TGCCTGCGAG CAGTCATTTT 2750
TTCCTAAAG TTTACAAGTA TTTAGAACTC TTCAGTTCAG GGCAAAATGT TCATGAAGTT 2810
ATTCTCTTA AACATGGTTA GGAAGCTGAT GACGTTATTG ATTTGTCTG GATTATGTTT 2870
10 CTGGAATAAT TTACCAAAAA CAAGCTATTT GAGTTTTGAC TTGACAAGGC AAAACATGAC 2930
AGTGGATTCT CTTTACAAAT TGAAAAAATA AATCCTTATT TTGTATAAAG GACTTCCCTT 2990
TTTGTAACCT AATCCTTTTT ATTGGTAAAA ATTGTAAATT AAAATGTGCA ACTTG 3045

```

15 (2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

20 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

25 (B) CELL KIND: Epidermoid carcinoma

(C) CELL LINE: KB

(D) CLONE NAME: HP10389

(ix) SEQUENCE CHARACTERISTICS:

30 (A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 63.. 383

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

35

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ATGACCTTCA CCGGGAGGCT GAGGTCGGAG TCCCGATTTT CTCCTGCTGC TGTGGCCCGG 60
AC ATG GCG ACT CCC GGC CCT GTG ATT CCG GAG GTC CCC TTT GAA CCA 107
Met Ala Thr Pro Gly Pro Val Ile Pro Glu Val Pro Phe Glu Pro

```

	1	5	10	15	
	TCG AAG CCT CCA GTC ATT GAG GGG CTG AGC CCC ACT GTT TAC AGG AAT				155
	Ser Lys Pro Pro Val Ile Glu Gly Leu Ser Pro Thr Val Tyr Arg Asn				
		20	25	30	
5	CCA GAG AGT TTC AAG GAA AAG TTC GTT CGC AAG ACC CGC GAG AAC CCG				203
	Pro Glu Ser Phe Lys Glu Lys Phe Val Arg Lys Thr Arg Glu Asn Pro				
		35	40	45	
	GTG GTA CCC ATA GGT TGC CTG GCC ACG GCG GCC GCC CTC ACC TAC GGC				251
	Val Val Pro Ile Gly Cys Leu Ala Thr Ala Ala Ala Leu Thr Tyr Gly				
10		50	55	60	
	CTC TAC TCC TTC CAC CGG GGC AAC AGC CAG CGC TCT CAG CTC ATG ATG				299
	Leu Tyr Ser Phe His Arg Gly Asn Ser Gln Arg Ser Gln Leu Met Met				
		65	70	75	
	CGC ACC CGG ATC GCC GCC CAG GGT TTC ACG GTC GCA GCC ATC TTG CTG				347
15	Arg Thr Arg Ile Ala Ala Gln Gly Phe Thr Val Ala Ala Ile Leu Leu				
		80	85	90	95
	GGT CTG GCT GTC ACT GCT ATG AAG TCT CGA CCC TAAGCCCAGG GTCTGGCCTT				400
	Gly Leu Ala Val Thr Ala Met Lys Ser Arg Pro				
		100	105		
20	GAAAGCTCCG CAGAAATGAT TCCAAAACCC AGGGAGCAAC CACTGGCCCT ACCGTGGGAC				460
	TTACTCCCTC CTCTCCTTTG AGAGGCCCAT GTGTCGTGG GGAGGAAGTG ACCCTTTGTG				520
	TAAGTGTAA CGAAAGTTTT TTCAAAAATC CTAGATGCTG TTGTTTGAAT GTTACATACT				580
	TCTATTTTGT CCACATCTCC CCTCCACTCC CTGCTTAAT AAAGCTCTAA AATCCACTTG				640
	TATTTAATTC AGT				653

25

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439

30

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

35

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10408

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 75.. 311

(C) CHARACTERIZATION METHOD: E

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

```

GTAGAAACAG GCCTGTTAAG GAGAGGCCAC CGGGACTTCA GTGTCTCCTC CATCCCAGGA      60
GCGCAGTGGC CACT ATG GGG TCT GGG CTG CCC CTT GTC CTC CTC TTG ACC      110
10      Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr
           1               5               10
CTC CTT GGC AGC TCA CAT GGA ACA GGG CCG GGT ATG ACT TTG CAA CTC      158
Leu Leu Gly Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu
           15               20               25
15 AAG CTG AAG GAG TCT TTT CTG ACA AAT TCC TCC TAT GAG TCC AGC TTC      206
Lys Leu Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe
           30               35               40
CTG GAA TTG CTT GAA AAG CTC TGC CTC CTC CTC CAT CTC CCT TCA GGG      254
Leu Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
20  45               50               55               60
ACC AGC GTC ACC CTC CAC CAT GCA AGA TCT CAA CAC CAT GTT GTC TGC      302
Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val Cys
           65               70               75
AAC ACA TGACAGCCAT TGAAGCCTGT GTCCTTCTTG GCCCGGGCTT TTGGCCCGGG GA      360
25 Asn Thr

TGCAGGAGGC AGGCCCGGAC CCTGTCTTTC AGCAGGCCCC CACCCTCCTG AGTGCCAATA      420
AATAAAATTC GGTATGCTG                                         439

```

30

## (2) INFORMATION FOR SEQ ID NO: 45:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1131

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10412

5

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 56.. 1000  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

	CTATGAGATC CCGGCCTCAG GGTGGACGCA GTGGTTCTGC ACTGAGGCCC TCGTC ATG	58
		Met
15		1
	GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT	106
	Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe	
	5 10 15	
	ATC CTC TTC CTG ACT CGC AGC CCG GGC CGG GCG GCA TCA GCC GGC CAA	154
20	Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln	
	20 25 30	
	GAG CCA CTG CAC AAT GAG GAG CTG GCA GGA GCA GGC CGG GTG GCC CAG	202
	Glu Pro Leu His Asn Glu Glu Leu Ala Gly Ala Gly Arg Val Ala Gln	
	35 40 45	
25	CCT GGG CCC CTG GAG CCT GAG GAG CCG AGA GCT GGA GGC AGG CCT CGG	250
	Pro Gly Pro Leu Glu Pro Glu Glu Pro Arg Ala Gly Gly Arg Pro Arg	
	50 55 60 65	
	CGC CGG AGG GAC CTG GGC AGC CGC CTA CAG GCC CAG CGT CGA GCC CAG	298
	Arg Arg Arg Asp Leu Gly Ser Arg Leu Gln Ala Gln Arg Arg Ala Gln	
30	70 75 80	
	CGG GTG GCC TGG GCA GAA GCA GAT GAG AAC GAG GAG GAA GCT GTC ATC	346
	Arg Val Ala Trp Ala Glu Ala Asp Glu Asn Glu Glu Glu Ala Val Ile	
	85 90 95	
	CTA GCC CAG GAG GAG GAA GGT GTC GAG AAG CCA GCG GAA ACT CAC CTG	394
35	Leu Ala Gln Glu Glu Glu Gly Val Glu Lys Pro Ala Glu Thr His Leu	
	100 105 110	
	TCG GGG AAA ATT GGA GCT AAG AAA CTG CGG AAG CTG GAG GAG AAA CAA	442
	Ser Gly Lys Ile Gly Ala Lys Lys Leu Arg Lys Leu Glu Glu Lys Gln	

	115	120	125	
	GCG CGA AAG GCC CAG CGT GAG GCA GAG GAG GCT GAA CGT GAG GAG CGG			490
	Ala Arg Lys Ala Gln Arg Glu Ala Glu Glu Ala Glu Arg Glu Glu Arg			
	130	135	140	145
5	AAA CGA CTC GAG TCC CAG CGC GAA GCT GAG TGG AAG AAG GAG GAG GAG			538
	Lys Arg Leu Glu Ser Gln Arg Glu Ala Glu Trp Lys Lys Glu Glu Glu			
	150	155	160	
	CGG CTT CGC CTG GAG GAG GAG CAG AAG GAG GAG GAG AGG AAG GCC			586
	Arg Leu Arg Leu Glu Glu Glu Gln Lys Glu Glu Glu Glu Arg Lys Ala			
10	165	170	175	
	CGC GAG GAG CAG GCC CAG CGG GAG CAT GAG GAG TAC CTG AAA CTG AAG			634
	Arg Glu Glu Gln Ala Gln Arg Glu His Glu Glu Tyr Leu Lys Leu Lys			
	180	185	190	
	GAG GCC TTT GTG GTG GAG GAG GAA GGC GTA GGA GAG ACC ATG ACT GAG			682
15	Glu Ala Phe Val Val Glu Glu Glu Gly Val Gly Glu Thr Met Thr Glu			
	195	200	205	
	GAA CAG TCC CAG AGC TTC CTG ACA GAG TTC ATC AAC TAC ATC AAG CAG			730
	Glu Gln Ser Gln Ser Phe Leu Thr Glu Phe Ile Asn Tyr Ile Lys Gln			
	210	215	220	225
20	TCC AAG GTT GTG CTC TTG GAA GAC CTG GCT TCC CAG GTG GGC CTA CGC			778
	Ser Lys Val Val Leu Leu Glu Asp Leu Ala Ser Gln Val Gly Leu Arg			
	230	235	240	
	ACT CAG GAC ACC ATA AAT CGC ATC CAG GAC CTG CTG GCT GAG GGG ACT			826
	Thr Gln Asp Thr Ile Asn Arg Ile Gln Asp Leu Leu Ala Glu Gly Thr			
25	245	250	255	
	ATA ACA GGT GTG ATT GAC GAC CGG GGC AAG TTC ATC TAC ATA ACC CCA			874
	Ile Thr Gly Val Ile Asp Asp Arg Gly Lys Phe Ile Tyr Ile Thr Pro			
	260	265	270	
	GAG GAA CTG GCC GCC GTG GCC AAC TTC ATC CGA CAG CGG GGC CGG GTG			922
30	Glu Glu Leu Ala Ala Val Ala Asn Phe Ile Arg Gln Arg Gly Arg Val			
	275	280	285	
	TCC ATC GCC GAG CTT GCC CAA GCC AGC AAC TCC CTC ATC GCC TGG GGC			970
	Ser Ile Ala Glu Leu Ala Gln Ala Ser Asn Ser Leu Ile Ala Trp Gly			
	290	295	300	305
35	CGG GAG TCC CCT GCC CAA GCC CCA GCC TGACCCAGT CCTTCCCTCT TGG			1020
	Arg Glu Ser Pro Ala Gln Ala Pro Ala			
	310			
	ACTCAGAGTT GGTGTGGCCT ACCTGGCTAT ACATCTTCAT CCCTCCCCAC CATCCTGGGG			1080

AAGTGATGGT GTGGCCAGGC AGTTATAGAT TAAAGGCCTG TGAGTACTGC T

1131

## (2) INFORMATION FOR SEQ ID NO: 46:

## 5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1875

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

## 10 (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

## 15 (D) CLONE NAME: HP10413

## (ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

(B) EXISTENCE POSITION: 79.. 666

## 20 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	CTCGCTCGCT CAGAGGGAGG AGAAAGTGGC GAGTTCCGGA TCCCTGCCTA GCGCGGCCCA	60
25	ACCTTTACTC CAGAGATC ATG GCT GCC GAG GAT GTG GTG GCG ACT GGC GCC	111
	Met Ala Ala Glu Asp Val Val Ala Thr Gly Ala	
	1 5 10	
	GAC CCA AGC GAT CTG GAG AGC GGC GGG CTG CTG CAT GAG ATT TTC ACG	159
	Asp Pro Ser Asp Leu Glu Ser Gly Gly Leu Leu His Glu Ile Phe Thr	
30	15 20 25	
	TCG CCG CTC AAC CTG CTG CTG CTT GGC CTC TGC ATC TTC CTG CTC TAC	207
	Ser Pro Leu Asn Leu Leu Leu Leu Cys Ile Phe Leu Leu Tyr	
	30 35 40	
	AAG ATC GTG GCG GGC GAC CAG CCG GCG GCC AGC GGC GAC AGC GAC GAC	255
35	Lys Ile Val Arg Gly Asp Gln Pro Ala Ala Ser Gly Asp Ser Asp Asp	
	45 50 55	
	GAC GAG CCG CCC CCT CTG CCC GCG CTC AAG CGG GCG GAC TTC ACC CCC	303
	Asp Glu Pro Pro Pro Leu Pro Arg Leu Lys Arg Arg Asp Phe Thr Pro	



	60	65	70	75	
	GCC GAG CTG CGG CGC TTC GAC GGC GTC CAG GAC CCG CGC ATA CTC ATG				351
	Ala Glu Leu Arg Arg Phe Asp Gly Val Gln Asp Pro Arg Ile Leu Met				
		80	85	90	
5	GCC ATC AAC GGC AAG GTG TTC GAT GTG ACC AAA GGC CGC AAA TTC TAC				399
	Ala Ile Asn Gly Lys Val Phe Asp Val Thr Lys Gly Arg Lys Phe Tyr				
		95	100	105	
	GGG CCC GAG GGG CCG TAT GGG GTC TTT GCT GGA AGA GAT GCA TCC AGG				447
	Gly Pro Glu Gly Pro Tyr Gly Val Phe Ala Gly Arg Asp Ala Ser Arg				
10		110	115	120	
	GGC CTT GCC ACA TTT TGC CTG GAT AAG GAA GCA CTG AAG GAT GAG TAC				495
	Gly Leu Ala Thr Phe Cys Leu Asp Lys Glu Ala Leu Lys Asp Glu Tyr				
		125	130	135	
	GAT GAC CTT TCT GAC CTC ACT GCT GCC CAG CAG GAG ACT CTG AGT GAC				543
15	Asp Asp Leu Ser Asp Leu Thr Ala Ala Gln Gln Glu Thr Leu Ser Asp				
		140	145	150	155
	TGG GAG TCT CAG TTC ACT TTC AAG TAT CAT CAC GTG GGC AAA CTG CTG				591
	Trp Glu Ser Gln Phe Thr Phe Lys Tyr His Val Gly Lys Leu Leu				
		160	165	170	
20	AAG GAG GGG GAG GAG CCC ACT GTG TAC TCA GAT GAG GAA GAA CCA AAA				639
	Lys Glu Gly Glu Glu Pro Thr Val Tyr Ser Asp Glu Glu Glu Pro Lys				
		175	180	185	
	GAT GAG AGT GCC CGG AAA AAT GAT TAAAGCATTC AGTGAAGTA TATCTAT				690
	Asp Glu Ser Ala Arg Lys Asn Asp				
25		190	195		
	TTTTGTATTT TGCAAAATCA TTTGTAACAG TCCACTCTGT CTTTAAACA TAGTGATTAC				750
	AATATTAGA AAGTTTGTAG CACTTGCTAT AAGTTTTTTA TAACATCACT AGTGACACTA				810
	ATAAAATTAA CTTCTTAGAA TGCATGATGT GTTTGTGTGT CACAAATCCA GAAAGTGAAC				870
	TGCAGTGTCT TAATACACAT GTTAATACTG TTTTCTTCT ATCTGTAGTT AGTACAGGAT				930
30	GAATTTAAAT GTGTTTTTCC TGAGAGACAA GGAAGACTTG GGTATTTCCC AAAACAGGTA				990
	AAAATCTTAA ATGTGCACCA AGAGCAAAGG ATCAACTTTT AGTCATGATG TTCTGTAAAG				1050
	ACAACAAATC CCTTTTTTTT TCTCAATTGA CTTAAGTGA TGATTTCTGT TTTATCTACC				1110
	TCTAAAGCAA ATCTGCAGTG TTCCAAAGAC TTTGGTATGG ATTAAGCGCT GTCCAGTAAC				1170
	AAAATGAAAT CTCAAAACAG AGCTCAGCTG CAAAAAGCA TATTTCTGT GTTCTGGAC				1230
35	TGCACTGTTG TCCITGCCCT CACATAGACA CTCAGACACC CTCACAAACA CAGTAGTCTA				1290
	TAGTTAGGAT TAAATAGGA TCTGAACATT CAAAAGAAAG CTTTGGAAAA AAAGAGCTGG				1350
	CTGGCCTAAA AACCTAAATA TATGATGAAG ATTGTAGGAC TGTCTTCCCA AGCCCCATGT				1410
	TCATGCTGGG GCAATGGTTA TTTGGTTATT TTAAGCAATT GGTACTCTC ATTTGAAATG				1470

AGGGAGGGAC ATACAGAATA GGAACAGGTG TTTGCTCTCC TAAGAGCCTT CATGCACACC 1530  
 CCTGAACCAC GAGGAAACAG TACAGTCGCT AGTCAAGTGG TTTTAAAGT AAAGTATATT 1590  
 CATAAGGTAA CAGTTATCT GTTGTATATA AACTATACCC ACTGCAAAAG TAGTAGCAA 1650  
 GTGTCTAGGT CTTTGATATT GCTCTTTTGG TTAACACTAA GCTTAAGTAG ACTATACAGT 1710  
 5 TGTATGAATT TGTAAGTA TATGAACACC TACTGAGATT TCAAAGTGT AATTGTGGTT 1770  
 AAATAGTCAT TGTATTTCT TGTGAAGTGT GTTTATGAT TTTACCTCA ATCAGAAAAC 1830  
 AAAATGATGT GCTTGGTCA GTTAATAAAA ATGGTTTAC CCACT 1875

10 (2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1563  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

15

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10415

20

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 72.. 1460  
 (C) CHARACTERIZATION METHOD: E

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

30 AAATTGGGCC AGGCTGAGGC GCTGCTGCTG GAGCGGCCGA TCCGAGACCT GGCTCCCTGG 60  
 GCGGCAGAAC C ATG TTG GAC TTC GCG ATC TTC GCC GTT ACC TTC TTG CTG 110  
 Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu  
 1 5 10  
 GCG TTG GTG GGA GCC GTG CTC TAC CTC TAT CCG GCT TCC AGA CAA GCT 158  
 35 Ala Leu Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala  
 15 20 25  
 GCA GGA ATT CCA GGG ATT ACT CCA ACT GAA GAA AAA GAT GGT AAT CTT 206  
 Ala Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu

	30		35		40		45										
	CCA	GAT	ATT	GTG	AAT	AGT	GGA	AGT	TTG	CAT	GAG	TTC	CTG	GTT	AAT	TTG	254
	Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn	Leu	
				50						55					60		
5	CAT	GAG	AGA	TAT	GGG	CCT	GTG	GTC	TCC	TTC	TGG	TTT	GGC	AGG	CGC	CTC	302
	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg	Arg	Leu	
				65					70					75			
	GTG	GTT	AGT	TTG	GGC	ACT	GTT	GAT	GTA	CTG	AAG	CAG	CAT	ATC	AAT	CCC	350
	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His	Ile	Asn	Pro	
10			80						85					90			
	AAT	AAG	ACA	TTG	GAC	CCT	TTT	GAA	ACC	ATG	CTG	AAG	TCA	TTA	TTA	AGG	398
	Asn	Lys	Thr	Leu	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys	Ser	Leu	Leu	Arg	
			95				100					105					
	TAT	CAA	TCT	GGT	GGT	GGC	AGT	GTG	AGT	GAA	AAC	CAC	ATG	AGG	AAA	AAA	446
15	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn	His	Met	Arg	Lys	Lys	
	110					115					120				125		
	TTG	TAT	GAA	AAT	GGT	GTG	ACT	GAT	TCT	CTG	AAG	AGT	AAC	TTT	GCC	CTC	494
	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu	Lys	Ser	Asn	Phe	Ala	Leu	
				130						135				140			
20	CTC	CTA	AAG	CTT	TCA	GAA	GAA	TTA	TTA	GAT	AAA	TGG	CTC	TCC	TAC	CCA	542
	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	Asp	Lys	Trp	Leu	Ser	Tyr	Pro	
				145						150				155			
	GAG	ACC	CAG	CAC	GTG	CCC	CTC	AGC	CAG	CAT	ATG	CTT	GGT	TTT	GCT	ATG	590
	Glu	Thr	Gln	His	Val	Pro	Leu	Ser	Gln	His	Met	Leu	Gly	Phe	Ala	Met	
25			160						165					170			
	AAG	TCT	GTT	ACA	CAG	ATG	GTA	ATG	GGT	AGT	ACA	TTT	GAA	GAT	GAT	CAG	638
	Lys	Ser	Val	Thr	Gln	Met	Val	Met	Gly	Ser	Thr	Phe	Glu	Asp	Asp	Gln	
			175				180					185					
	GAA	GTC	ATT	CGC	TTC	CAG	AAG	AAT	CAT	GGC	ACA	GTT	TGG	TCT	GAG	ATT	686
30	Glu	Val	Ile	Arg	Phe	Gln	Lys	Asn	His	Gly	Thr	Val	Trp	Ser	Glu	Ile	
	190					195					200				205		
	GGA	AAA	GGC	TTT	CTA	GAT	GGG	TCA	CTT	GAT	AAA	AAC	ATG	ACT	CGG	AAA	734
	Gly	Lys	Gly	Phe	Leu	Asp	Gly	Ser	Leu	Asp	Lys	Asn	Met	Thr	Arg	Lys	
				210						215				220			
35	AAA	CAA	TAT	GAA	GAT	GCC	CTC	ATG	CAA	CTG	GAG	TCT	GTT	TTA	AGG	AAC	782
	Lys	Gln	Tyr	Glu	Asp	Ala	Leu	Met	Gln	Leu	Glu	Ser	Val	Leu	Arg	Asn	
				225						230				235			
	ATC	ATA	AAA	GAA	CGA	AAA	GGA	AGG	AAC	TTC	AGT	CAA	CAT	ATT	TTC	ATT	830

	Ile	Ile	Lys	Glu	Arg	Lys	Gly	Arg	Asn	Phe	Ser	Gln	His	Ile	Phe	Ile	
			240					245					250				
	GAC	TCC	TTA	GTA	CAA	GGG	AAC	CTT	AAT	GAC	CAA	CAG	ATC	CTA	GAA	GAC	878
	Asp	Ser	Leu	Val	Gln	Gly	Asn	Leu	Asn	Asp	Gln	Gln	Ile	Leu	Glu	Asp	
5			255				260					265					
	AGT	ATG	ATA	TTT	TCT	CTG	GCC	AGT	TGC	ATA	ATA	ACT	GCA	AAA	TTG	TGT	926
	Ser	Met	Ile	Phe	Ser	Leu	Ala	Ser	Cys	Ile	Ile	Thr	Ala	Lys	Leu	Cys	
			270				275					280				285	
	ACC	TGG	GCA	ATC	TGT	TTT	TTA	ACC	ACC	TCT	GAA	GAA	GTT	CAA	AAA	AAA	974
10	Thr	Trp	Ala	Ile	Cys	Phe	Leu	Thr	Thr	Ser	Glu	Glu	Val	Gln	Lys	Lys	
					290					295					300		
	TTA	TAT	GAA	GAG	ATA	AAC	CAA	GTT	TTT	GGA	AAT	GGT	CCT	GTT	ACT	CCA	1022
	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val	Thr	Pro	
			305						310					315			
15	GAG	AAA	ATT	GAG	CAG	CTC	AGA	TAT	TGT	CAG	CAT	GTG	CTT	TGT	GAA	ACT	1070
	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu	Cys	Glu	Thr	
			320				325					330					
	GTT	CGA	ACT	GCC	AAA	CTG	ACT	CCA	GTT	TCT	GCC	CAG	CTT	CAA	GAT	ATT	1118
	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln	Leu	Gln	Asp	Ile	
20			335				340					345					
	GAA	GGA	AAA	ATT	GAC	CGA	TTT	ATT	ATT	CCT	AGA	GAG	ACC	CTC	GTC	CTT	1166
	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg	Glu	Thr	Leu	Val	Leu	
			350				355					360				365	
	TAT	GCC	CTT	GGT	GTG	GTA	CTT	CAG	GAT	CCT	AAT	ACT	TGG	CCA	TCT	CCA	1214
25	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro	Asn	Thr	Trp	Pro	Ser	Pro	
					370					375					380		
	CAC	AAG	TTT	GAT	CCA	GAT	CGG	TTT	GAT	GAT	GAA	TTA	GTA	ATG	AAA	ACT	1262
	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp	Asp	Glu	Leu	Val	Met	Lys	Thr	
			385				390					395					
30	TTT	TCC	TCA	CTT	GGA	TTC	TCA	GGC	ACA	CAG	GAG	TGT	CCA	GAG	TTG	AGG	1310
	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly	Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	
			400				405					410					
	TTT	GCA	TAT	ATG	GTG	ACC	ACA	GTA	CTT	CTT	AGT	GTA	TTG	GTG	AAG	AGA	1358
	Phe	Ala	Tyr	Met	Val	Thr	Thr	Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	
35			415				420					425					
	CTG	CAC	CTA	CTT	TCT	GTG	GAG	GGA	CAG	GTT	ATT	GAA	ACA	AAG	TAT	GAA	1406
	Leu	His	Leu	Leu	Ser	Val	Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	
	430					435					440					445	

CTG GTA ACA TCA TCA AGG GAA GAA GCT TGG ATC ACT GTC TCA AAG AGA 1454  
 Leu Val Thr Ser Ser Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg

450

455

460

TAT TAAAATTTTA TACATTTAAA ATCATTGTGA AATTGATTGA GGAAACAAC CAT 1510

5 Tyr

TTAAAAA TCTATGTTGA ATCCTTTTAT AAACCAGTAT CACTTTGTAA TAT 1563

10 (2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2030

(B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

15 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

20 (B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10419

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS

25 (B) EXISTENCE POSITION: 171.. 914

(C) CHARACTERIZATION METHOD: E

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

30 CATTGGGGT TTCGGTCCG CCCCTTCCCG TTCCCGGGG TCTGGGGGTG ACATTGCACC 60

GCGCCCTCG TGGGTCGCG TTGCCACCC AGCGGACTC CCCAGCTGGC GCGCCCTCC 120

CATTGCCTG TCCTGGTCAG GCGCCACCC CCCTTCCAC CTGACCAGCC ATG GGG 176

Met Gly

1

35 GCT GCG GTG TTT TTC GGC TGC ACT TTC GTC GCG TTC GGC CCG GCC TTC 224

Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe Gly Pro Ala Phe

5

10

15

GCG CTT TTC TTG ATC ACT GTG GCT GGG GAC CCG CTT CGC GTT ATC ATC 272

	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	Leu	Arg	Val	Ile	Ile	
	20						25					30					
	CTG	GTC	GCA	GGG	GCA	TTT	TTC	TGG	CTG	GTC	TCC	CTG	CTC	CTG	GCC	TCT	320
	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	Leu	Leu	Leu	Ala	Ser	
5	35					40					45				50		
	GTG	GTC	TGG	TTC	ATC	TTG	GTC	CAT	GTG	ACC	GAC	CGG	TCA	GAT	GCC	CGG	368
	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	Asp	Arg	Ser	Asp	Ala	Arg	
					55					60					65		
	CTC	CAG	TAC	GGC	CTC	CTG	ATT	TTT	GGT	GCT	GCT	GTC	TCT	GTC	CTT	CTA	416
10	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	Ala	Ala	Val	Ser	Val	Leu	Leu	
				70					75					80			
	CAG	GAG	GTG	TTC	CGC	TTT	GCC	TAC	TAC	AAG	CTG	CTT	AAG	AAG	GCA	GAT	464
	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	
				85				90						95			
15	GAG	GGG	TTA	GCA	TCG	CTG	AGT	GAG	GAC	GGA	AGA	TCA	CCC	ATC	TCC	ATC	512
	Glu	Gly	Leu	Ala	Ser	Leu	Ser	Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	
		100				105						110					
	CGC	CAG	ATG	GCC	TAT	GTT	TCT	GGT	CTC	TCC	TTC	GGT	ATC	ATC	AGT	GGT	560
	Arg	Gln	Met	Ala	Tyr	Val	Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	
20	115					120					125				130		
	GTC	TTC	TCT	GTT	ATC	AAT	ATT	TTG	GCT	GAT	GCA	CTT	GGG	CCA	GGT	GTG	608
	Val	Phe	Ser	Val	Ile	Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	
					135					140					145		
	GTT	GGG	ATC	CAT	GGA	GAC	TCA	CCC	TAT	TAC	TTC	CTG	ACT	TCA	GCC	TTT	656
25	Val	Gly	Ile	His	Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	
				150						155					160		
	CTG	ACA	GCA	GCC	ATT	ATC	CTG	CTC	CAT	ACC	TTT	TGG	GGA	GTT	GTG	TTC	704
	Leu	Thr	Ala	Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	
				165				170						175			
30	TTT	GAT	GCC	TGT	GAG	AGG	AGA	CGG	TAC	TGG	GCT	TTG	GGC	CTG	GTG	GTT	752
	Phe	Asp	Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	
				180				185					190				
	GGG	AGT	CAC	CTA	CTG	ACA	TCG	GGA	CTG	ACA	TTC	CTG	AAC	CCC	TGG	TAT	800
	Gly	Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	
35	195					200					205				210		
	GAG	GCC	AGC	CTG	CTG	CCC	ATC	TAT	GCA	GTC	ACT	GTT	TCC	ATG	GGG	CTC	848
	Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	Leu	
					215					220					225		

TGG GCC TTC ATC ACA GCT GGA GGG TCC CTC CGA AGT ATT CAG CGC AGC 896  
 Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser Ile Gln Arg Ser  
 230 235 240  
 CTC TTG TGT AAG GAC TGA CTACCTG GACTGATCGC CTGACAGATC CCACCTGCC 950  
 5 Leu Leu Cys Lys Asp  
 245  
 TGTCCACTGC CCATGACTGA GCCCAGCCCC AGCCCGGGTC CATTGCCAC ATTCTCTGTC 1010  
 TCCTTCTCGT CGGTCTACCC CACTACCTCC AGGGTTTTGC TTTGTCTCTT TGTGACCGTT 1070  
 AGTCTCTAAG CTTTACCAGG AGCAGCCTGG GTTCAGCCAG TCAGTGACTG GTGGGTTTGA 1130  
 10 ATCTGCACCT ATCCCCACCA CCTGGGGACC CCCTTGTTGT GTCCAGGACT CCCCTGTGT 1190  
 CAGTGCTCTG CTCTACCCCT GCCCAAGACT CACCTCCCTT CCCCTCTGCA GGCCGACGGC 1250  
 AGGAGGACAG TCGGGTGATG GTGTATTCTG CCCTGCGCAT CCCACCCGAG GACTGAGGGA 1310  
 ACCTAGGGGG GACCCCTGGG CCTGGGGTGC CCTCCTGATG TCCTCGCCCT GTATTTCTCC 1370  
 ATCTCCAGTT CTGACAGATG CAGGTTGCCA AGAAAAGGGA CCTAGTTTAG CCATTGCCCT 1430  
 15 GGAGATGAAA TTAATGGAGG CTCAAGGATA GATGAGCTCT GAGTTTCTCA GTACTCCCTC 1490  
 AAGACTGGAC ATCTTGGTCT TTTTCTCAGG CCTGAGGGGG AACCATTTTT GGTGTGATAA 1550  
 ATACCCTAAA CTGCCTTTTT TTCTTTTTTG AGGTGGGGGG AGGGAGGAGG TATATTGGAA 1610  
 CTCTTCTAAC CTCCTTGGGC TATATTTCT CTCTCGAGT TGCTCCTCAT GGCTGGGCTC 1670  
 ATTTGCTGCC CTTTCTCCTT GGTCCAGAC CTGGGGGAA AGGAAGGAAG TGCATGTTTG 1730  
 20 GGAAGTGCCA TTA CTGGAAC TAATGGTTTT AACCTCCTTA ACCACCAGCA TCCCTCCTCT 1790  
 CCCCAGGTG AAGTGGAGGG TGCTGTGGTG AGCTGGCCAC TCCAGAGCTG CAGTGCCACT 1850  
 GGAGGAGTCA GACTACCATG ACATCGTAGG GAAGGAGGGG AGATTTTTTT TAGTTTTTTA 1910  
 ATTGGGTGT GGGAGGGGCG GGGAGGTTTT CTATAAACTG TATCATTTT TGCTGAGGGT 1970  
 GGAGTGTCCT ATCCTTTTAA TCAAGGTGAT TGTGATTTTG ACTAATAAAA AAGAATTTGT 2030  
 25

## (2) INFORMATION FOR SEQ ID NO: 49:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493

30 (B) TYPE: Nucleic acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

## 35 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*

(B) CELL KIND: Stomach cancer

(D) CLONE NAME: HP10424

(A) LENGTH: 2044



(B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA

5

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Epidermoid carcinoma  
 (C) CELL LINE: KB  
 (D) CLONE NAME: HP10428

10

(ix) SEQUENCE CHARACTERISTICS:

(A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 288.. 1385  
 (C) CHARACTERIZATION METHOD: E

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

	AGATTCCGGC CTGGAGCTCC CAGGGCCGAG CAGACCTTGG GACCTGTGAG CGCTGCATCC	60
20	AATTAACCAT GGGAAGGGTC AGCACCAGCC ACCAGCCCCT TAGGTGAGGA CTCTGCCTGG	120
	GGCTCTGCTG ATGGTTCCGA ATCATGGAGC TGCAGAGAGC TCCTCCAGCC TGGAGACGTT	180
	CTTGGTGAAA GCTGTGGTCT AACTCCACCG GCTCTTCCTG CACATTGTAT TCAAGAGGGG	240
	TGCCTGCCCC CGCTGACTCA GGAGCTCCGG TGCTGCAGCC GCCACGA ATG GGG AGG	296
		Met Gly Arg
25		1
	TGG GCC CTC GAT GTG GCC TTT TTG TGG AAG GCG GTG TTG ACC CTG GGG	344
	Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu Thr Leu Gly	
	5 10 15	
	CTG GTG CTT CTC TAC TAC TGC TTC TCC ATC GGC ATC ACC TTC TAC AAC	392
30	Leu Val Leu Leu Tyr Tyr Cys Phe Ser Ile Gly Ile Thr Phe Tyr Asn	
	20 25 30 35	
	AAG TGG CTG ACA AAG AGC TTC CAT TTC CCC CTC TTC ATG ACG ATG CTG	440
	Lys Trp Leu Thr Lys Ser Phe His Phe Pro Leu Phe Met Thr Met Leu	
	40 45 50	
35	CAC CTG GCC GTG ATC TTC CTC TTC TCC GCC CTG TCC AGG GCG CTG GTT	488
	His Leu Ala Val Ile Phe Leu Phe Ser Ala Leu Ser Arg Ala Leu Val	
	55 60 65	
	CAG TGC TCC AGC CAC AGG GCC CGT GTG GTG CTG AGC TGG GCC GAC TAC	536

	Gln	Cys	Ser	Ser	His	Arg	Ala	Arg	Val	Val	Leu	Ser	Trp	Ala	Asp	Tyr	
			70					75					80				
	CTC	AGA	AGA	GTG	GCT	CCC	ACA	GCT	CTG	GCG	ACG	GCG	CTT	GAC	GTG	GGC	584
	Leu	Arg	Arg	Val	Ala	Pro	Thr	Ala	Leu	Ala	Thr	Ala	Leu	Asp	Val	Gly	
5			85					90					95				
	TTG	TCC	AAC	TGG	AGC	TTC	CTG	TAT	GTC	ACC	GTC	TCG	CTG	TAC	ACA	ATG	632
	Leu	Ser	Asn	Trp	Ser	Phe	Leu	Tyr	Val	Thr	Val	Ser	Leu	Tyr	Thr	Met	
	100					105					110				115		
	ACC	AAA	TCC	TCA	GCT	GTC	CTC	TTC	ATC	TTG	ATC	TTC	TCT	CTG	ATC	TTC	680
10	Thr	Lys	Ser	Ser	Ala	Val	Leu	Phe	Ile	Leu	Ile	Phe	Ser	Leu	Ile	Phe	
					120					125					130		
	AAG	CTG	GAG	GAG	CTG	CGC	GCG	GCA	CTG	GTC	CTG	GTG	GTC	CTC	CTC	ATC	728
	Lys	Leu	Glu	Glu	Leu	Arg	Ala	Ala	Leu	Val	Leu	Val	Val	Leu	Leu	Ile	
					135				140					145			
15	GCC	GGG	GGT	CTC	TTC	ATG	TTC	ACC	TAC	AAG	TCC	ACA	CAG	TTC	AAC	GTG	776
	Ala	Gly	Gly	Leu	Phe	Met	Phe	Thr	Tyr	Lys	Ser	Thr	Gln	Phe	Asn	Val	
					150				155					160			
	GAG	GGC	TTC	GCC	TTG	GTG	CTG	GGG	GCC	TCG	TTC	ATC	GGT	GGC	ATT	CGC	824
	Glu	Gly	Phe	Ala	Leu	Val	Leu	Gly	Ala	Ser	Phe	Ile	Gly	Gly	Ile	Arg	
20			165				170					175					
	TGG	ACC	CTC	ACC	CAG	ATG	CTC	CTG	CAG	AAG	GCT	GAA	CTC	GGC	CTC	CAG	872
	Trp	Thr	Leu	Thr	Gln	Met	Leu	Leu	Gln	Lys	Ala	Glu	Leu	Gly	Leu	Gln	
	180					185					190				195		
	AAT	CCC	ATC	GAC	ACC	ATG	TTC	CAC	CTG	CAG	CCA	CTC	ATG	TTC	CTG	GGG	920
25	Asn	Pro	Ile	Asp	Thr	Met	Phe	His	Leu	Gln	Pro	Leu	Met	Phe	Leu	Gly	
					200					205				210			
	CTC	TTC	CCT	CTC	TTT	GCT	GTA	TTT	GAA	GGT	CTC	CAT	TTG	TCC	ACA	TCT	968
	Leu	Phe	Pro	Leu	Phe	Ala	Val	Phe	Glu	Gly	Leu	His	Leu	Ser	Thr	Ser	
					215				220					225			
30	GAG	AAA	ATC	TTC	CGT	TTC	CAG	GAC	ACA	GGG	CTG	CTC	CTG	CGG	GTA	CTT	1016
	Glu	Lys	Ile	Phe	Arg	Phe	Gln	Asp	Thr	Gly	Leu	Leu	Leu	Arg	Val	Leu	
					230				235					240			
	GGG	AGC	CTC	TTC	CTT	GGC	GGG	ATT	CTC	GCC	TTT	GGT	TTG	GGC	TTC	TCT	1064
	Gly	Ser	Leu	Phe	Leu	Gly	Gly	Ile	Leu	Ala	Phe	Gly	Leu	Gly	Phe	Ser	
35			245				250					255					
	GAG	TTC	CTC	CTG	GTC	TCC	AGA	ACC	TCC	AGC	CTC	ACT	CTC	TCC	ATT	GCC	1112
	Glu	Phe	Leu	Leu	Val	Ser	Arg	Thr	Ser	Ser	Leu	Thr	Leu	Ser	Ile	Ala	
	260					265					270				275		

	GGC ATT TTT AAG GAA GTC TGC ACT TTG CTG TTG GCA GCT CAT CTG CTG	1160
	Gly Ile Phe Lys Glu Val Cys Thr Leu Leu Leu Ala Ala His Leu Leu	
	280 285 290	
	GGC GAT CAG ATC AGC CTC CTG AAC TGG CTG GGC TTC GCC CTC TGC CTC	1208
5	Gly Asp Gln Ile Ser Leu Leu Asn Trp Leu Gly Phe Ala Leu Cys Leu	
	295 300 305	
	TCG GGA ATA TCC CTC CAC GTT GCC CTC AAA GCC CTG CAT TCC AGA GGT	1256
	Ser Gly Ile Ser Leu His Val Ala Leu Lys Ala Leu His Ser Arg Gly	
	310 315 320	
10	GAT GGT GGC CCC AAG GCC TTG AAG GGG CTG GGC TCC AGC CCC GAC CTG	1304
	Asp Gly Gly Pro Lys Ala Leu Lys Gly Leu Gly Ser Ser Pro Asp Leu	
	325 330 335	
	GAG CTG CTG CTC CGG AGC AGC CAG CGG GAG GAA GGT GAC AAT GAG GAG	1352
	Glu Leu Leu Leu Arg Ser Ser Gln Arg Glu Glu Gly Asp Asn Glu Glu	
15	340 345 350 355	
	GAG GAG TAC TTT GTG GCC CAG GGG CAG CAG TGACCAGCCA GGGCAAAT	1400
	Glu Glu Tyr Phe Val Ala Gln Gly Gln Gln	
	360 365	
	GGCTTAGAAG CAGGCCACTC CCCAGCCTGC TGCCAGCACT CACTGTGCTC AAGCCGCCAG	1460
20	GGCTCATCAT GGTAGCTGGG AGCTGTGGAC GGGAGTCACC AGGTGGTGGG GCCAAGCCAG	1520
	GGACTCATGA CTTTGGCCCC TCCCTTCAGA GCCTGTCTCAC ACAAGGGGCG AGCACCAGGC	1580
	CAGCCTGGGA CTGGCCAGAG CTGGGCCCAA GCTGCGCTGG AATCGCAGCA GGAGAGGGGA	1640
	GTGGGCTGGT TCTTCCCAACC ACTTCCCAGG CTCTGACAGC CGAGACTCAT TTCCAAGGCA	1700
	CAGCAGCTTT CTAAAGGGAC TGAGTTTGA CTGGGTTTTG GACCTCCAGG GGCTGGAGCT	1760
25	TCATCACCTG GGCAGTGTCT TTTCTCAGAG AGCAGGTTTC TTTATAGTTT GAAATAAAAT	1820
	GGTTCACGGT CCACTGGCCG CCTTGTGTG CTGGAGACGT GGGGGCAGGG AGGGACAGT	1880
	GTGGGCCCTG CCTCTCCTTT CCTTCCCTG CCTGGAGCCT TCTTCAAATG TCTGGTCTTA	1940
	AGCCAGGCCT CCTTCATTTT CTCGCTCCTG TTAGAACCAC AGTCCCTCC CAGTGGGGC	2000
	CCCACTGCAC CTGCTGCCAG GAAATAAATG AATGTTTACT GAGT	2044
30		

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1043
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10429

5

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 157.. 837  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

ATTAGCATAA CCCTTCCTCA GGAAGAGTGA GATTTTATAT TTGACAATAA AGTGTTAGAC      60
TCCATTCTCA AATACCAGAC TTCAAAAGAT AAGGTTCAAA AGTGTATATA GAAGATATTC      120
15 CTTTTTTTGT CCTAGAGAAC TTATTTTCT GTGAAA ATG CCT ACC ACA AAG AAG      174
                                     Met Pro Thr Thr Lys Lys
                                     1           5
ACA TTG ATG TTC TTA TCA AGC TTT TTC ACC AGC CTT GGG TCC TTC ATT      222
Thr Leu Met Phe Leu Ser Ser Phe Phe Thr Ser Leu Gly Ser Phe Ile
20           10           15           20
GTA ATT TGC TCT ATT CTT GGG ACA CAA GCA TGG ATC ACC AGT ACA ATT      270
Val Ile Cys Ser Ile Leu Gly Thr Gln Ala Trp Ile Thr Ser Thr Ile
           25           30           35
GCT GTT AGA GAC TCT GCT TCA AAT GGG AGC ATT TTC ATC ACT TAC GGA      318
25 Ala Val Arg Asp Ser Ala Ser Asn Gly Ser Ile Phe Ile Thr Tyr Gly
           40           45           50
CTT TTT CGT GGG GAG AGT AGT GAA GAA TTG AGT CAC GGA CTT GCA GAA      366
Leu Phe Arg Gly Glu Ser Ser Glu Glu Leu Ser His Gly Leu Ala Glu
           55           60           65           70
30 CCA AAG AAA AAG TTT GCA GTT TTA GAG ATA CTG AAT AAT TCT TCC CAA      414
Pro Lys Lys Lys Phe Ala Val Leu Glu Ile Leu Asn Asn Ser Ser Gln
           75           80           85
AAA ACT CTG CAT TCG GTG ACT ATC CTG TTC CTG GTC CTG AGT TTG ATC      462
Lys Thr Leu His Ser Val Thr Ile Leu Phe Leu Val Leu Ser Leu Ile
35           90           95           100
ACG TCG CTG CTG AGC TCT GGG TTT ACC TTC TAC AAC AGC ATC AGC AAC      510
Thr Ser Leu Leu Ser Ser Gly Phe Thr Phe Tyr Asn Ser Ile Ser Asn
           105           110           115

```

	CCT TAC CAG ACA TTC CTG GGG CCG ACG GGG GTG TAC ACC TGG AAC GGG	558
	Pro Tyr Gln Thr Phe Leu Gly Pro Thr Gly Val Tyr Thr Trp Asn Gly	
	120 125 130	
	CTC GGT GCA TCC TTC GTT TTT GTG ACC ATG ATA CTG TTT GTG GCG AAC	606
5	Leu Gly Ala Ser Phe Val Phe Val Thr Met Ile Leu Phe Val Ala Asn	
	135 140 145 150	
	ACG CAG TCC AAC CAA CTC TCC GAA GAG TTG TTC CAA ATG CTT TAC CCG	654
	Thr Gln Ser Asn Gln Leu Ser Glu Glu Leu Phe Gln Met Leu Tyr Pro	
	155 160 165	
10	GCA ACC ACC AGT AAA GGA ACG ACC CAC AGT TAC GGA TAC TCG TTC TGG	702
	Ala Thr Thr Ser Lys Gly Thr Thr His Ser Tyr Gly Tyr Ser Phe Trp	
	170 175 180	
	CTC ATA CTG CTC GTC ATT CTT CTA AAT ATA GTC ACT GTA ACC ATC ATC	750
	Leu Ile Leu Leu Val Ile Leu Leu Asn Ile Val Thr Val Thr Ile Ile	
15	185 190 195	
	ATT TTC TAC CAG AAG GCC AGA TAC CAG CGG AAG CAG GAG CAG AGA AAG	798
	Ile Phe Tyr Gln Lys Ala Arg Tyr Gln Arg Lys Gln Glu Gln Arg Lys	
	200 205 210	
	CCA ATG GAA TAT GCT CCA AGG GAC GGA ATT TTA TTC TGAATCTCT TTCATC	850
20	Pro Met Glu Tyr Ala Pro Arg Asp Gly Ile Leu Phe	
	215 220 225	
	TCATTTTGGC GTTGCACTTA TTGTACATCA GCCCTGAGTA GTAACTGGTT AGCTTCTCTG	910
	GACAATTCAG CATGGTAACG TGACTGTCTAT CTGTGACAGC ATTGTGTTT CATGACACTG	970
	TGTTCTTCAT TGATGCTGTA CTCCTGAAAA TTTTCCCAC AAGGTTGGGG AAATGAATGG	1030
25	GAAATGTCGC TGG	1043

## (2) INFORMATION FOR SEQ ID NO: 52:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 972  
 (B) TYPE: Nucleic acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

## (ii) SEQUENCE KIND: cDNA to mRNA

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Liver

(D) CLONE NAME: HP10432

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 5 (B) EXISTENCE POSITION: 29.. 418  
 (C) CHARACTERIZATION METHOD: E

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

```

10  AGACAGCGGC GGGCGCAGGA CGTGCACT ATG GCT CGG GGC TCG CTG CGC CGG      52
                                     Met Ala Arg Gly Ser Leu Arg Arg
                                     1           5
    TTG CTG CGG CTC CTC GTG CTG GGG CTC TGG CTG GCG TTG CTG CGC TCC      100
    Leu Leu Arg Leu Leu Val Leu Gly Leu Trp Leu Ala Leu Leu Arg Ser
15  10           15           20
    GTG GCC GGG GAG CAA GCG CCA GGC ACC GCC CCC TGC TCC CGC GGC AGC      148
    Val Ala Gly Glu Gln Ala Pro Gly Thr Ala Pro Cys Ser Arg Gly Ser
    25           30           35           40
    TCC TGG AGC GCG GAC CTG GAC AAG TGC ATG GAC TGC GCG TCT TGC AGG      196
20  Ser Trp Ser Ala Asp Leu Asp Lys Cys Met Asp Cys Ala Ser Cys Arg
    45           50           55
    GCG CGA CCG CAC AGC GAC TTC TGC CTG GGC TGC GCT GCA GCA CCT CCT      244
    Ala Arg Pro His Ser Asp Phe Cys Leu Gly Cys Ala Ala Ala Pro Pro
    60           65           70
25  GCC CCC TTC CGG CTG CTT TGG CCC ATC CTT GGG GGC GCT CTG AGC CTG      292
    Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu Gly Gly Ala Leu Ser Leu
    75           80           85
    ACC TTC GTG CTG GGG CTG CTT TCT GGC TTT TTG GTC TGG AGA CGA TGC      340
    Thr Phe Val Leu Gly Leu Leu Ser Gly Phe Leu Val Trp Arg Arg Cys
30  90           95           100
    CGC AGG AGA GAG AAG TTC ACC ACC CCC ATA GAG GAG ACC GGC GGA GAG      388
    Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile Glu Glu Thr Gly Gly Glu
    105          110          115          120
    GGC TGC CCA GCT GTG GCG CTG ATC CAG TGACA ATGT GCCCCTGCC A CCGG      440
35  Gly Cys Pro Ala Val Ala Leu Ile Gln
    125
    GGCTCGCCCA CTCATCATTC ATTCATCCAT TCTAGAGCCA GTCTCTGCCT CCCAGACGG      500
    GCGGGAGCCA AGCTCCTCCA ACCACAAGG GGGTGGGGG CGGTGAATCA CCTCTGAGGC      560
  
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CTGGGCCCAG GGTTCAGGGG AACCTTCCAA GGTGTCTGGT TGCCCTGGCT CTGGCTCCAG 620  
 AACAGAAAGG GAGCCTCAGC CTGGCTCACA CAAAACAGCT GACACTGACT AAGGAAGTGC 680  
 AGCATTGCA CAGGGGAGGG GGGTGCCCTC CTTCTAGAG GCCCTGGGGG CCAGGCTGAC 740  
 TTGGGGGGCA GACTTGACAC TAGGCCCCAC TCACTCAGAT GTCCTGAAAT TCCACCACGG 800  
 5 GGGTCACCCCT GGGGGGTTAG GGACCTATTT TTAACACTAG GGGGCTGGCC CACTAGGAGG 860  
 GCTGGCCCTA AGATACAGAC CCCCCCAACT CCCCAGGCG GGGAGGAGAT ATTTATTTTG 920  
 GGGAGAGTTT GGAGGGGAGG GAGAATTAT TAATAAAGA ATCTTAACT TT 972

10 (2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: Linear

15

(ii) SEQUENCE KIND: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*
- (B) CELL KIND: Liver
- (C) CELL LINE:
- (D) CLONE NAME: HP10433

20

(ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS
- (B) EXISTENCE POSITION: 73.. 564
- (C) CHARACTERIZATION METHOD: E

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

30

AAGATTTCAG CTGCGGGACG GTCAGGGGAG ACCTCCAGGC GCAGGGAAGG ACGGCCAGGG 60  
 TGACACGGAA GC ATG CGA CGG CTG CTG ATC CCT CTG GCC CTG TGG CTG GGC 111  
 Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly  
 1 5 10  
 35 GCG GTG GGC GTG GGC GTC GCC GAG CTC ACG GAA GCC CAG CGC CGG GGC 159  
 Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly  
 15 20 25  
 CTG CAG GTG GCC CTG GAG GAA TTT CAC AAG CAC CCG CCC GTG CAG TGG 207

	Leu	Gln	Val	Ala	Leu	Glu	Glu	Phe	His	Lys	His	Pro	Pro	Val	Gln	Trp	
	30				35					40						45	
	GCC	TTC	CAG	GAG	ACC	AGT	GTG	GAG	AGC	GCC	GTG	GAC	ACG	CCC	TTC	CCA	255
	Ala	Phe	Gln	Glu	Thr	Ser	Val	Glu	Ser	Ala	Val	Asp	Thr	Pro	Phe	Pro	
5					50					55						60	
	GCT	GGA	ATA	TTT	GTG	AGG	CTG	GAA	TTT	AAG	CTG	CAG	CAG	ACA	AGC	TGC	303
	Ala	Gly	Ile	Phe	Val	Arg	Leu	Glu	Phe	Lys	Leu	Gln	Gln	Thr	Ser	Cys	
					65					70						75	
	CGG	AAG	AGG	GAC	TGG	AAG	AAA	CCC	GAG	TGC	AAA	GTC	AGG	CCC	AAT	GGG	351
10	Arg	Lys	Arg	Asp	Trp	Lys	Lys	Pro	Glu	Cys	Lys	Val	Arg	Pro	Asn	Gly	
					80					85						90	
	AGG	AAA	CGG	AAA	TGC	CTG	GCC	TGC	ATC	AAA	CTG	GGC	TCT	GAG	GAC	AAA	399
	Arg	Lys	Arg	Lys	Cys	Leu	Ala	Cys	Ile	Lys	Leu	Gly	Ser	Glu	Asp	Lys	
					95					100						105	
15	GTT	CTG	GGC	CGG	TTG	GTG	CAC	TGC	CCC	ATA	GAG	ACC	CAA	GTT	CTG	CGG	447
	Val	Leu	Gly	Arg	Leu	Val	His	Cys	Pro	Ile	Glu	Thr	Gln	Val	Leu	Arg	
					110					115						125	
	GAG	GCT	GAG	GAG	CAC	CAG	GAG	ACC	CAG	TGC	CTC	AGG	GTG	CAG	CGG	GCT	495
	Glu	Ala	Glu	Glu	His	Gln	Glu	Thr	Gln	Cys	Leu	Arg	Val	Gln	Arg	Ala	
20					130					135						140	
	GGT	GAG	GAC	CCC	CAC	AGC	TTC	TAC	TTC	CCT	GGA	CAG	TTC	GCC	TTC	TCC	543
	Gly	Glu	Asp	Pro	His	Ser	Phe	Tyr	Phe	Pro	Gly	Gln	Phe	Ala	Phe	Ser	
					145					150						155	
	AAG	GCC	CTG	CCC	CGC	AGC	TAAGCCAGCA	CTGAGCTGCG	TGTTGCCTC								590
25	Lys	Ala	Leu	Pro	Arg	Ser											
					160												
	CAGGACCGCT	GCCGGTGGTA	ACCACTGGAA	GACCCAGCC	CCCAGGGAGA	GGACCCCGTT											650
	CTATCCCGAG	CCATGATAAT	AAAGCTGCTC	TCCCAGCTGC	CTCTC												695

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1914

(B) TYPE: Nucleic acid

35

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ii) SEQUENCE KIND: cDNA to mRNA



## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Homo sapiens*  
 (B) CELL KIND: Stomach cancer  
 (D) CLONE NAME: HP10480

5

## (ix) SEQUENCE CHARACTERISTICS:

- (A) CHARACTERIZATION CODE: CDS  
 (B) EXISTENCE POSITION: 80.. 661  
 (C) CHARACTERIZATION METHOD: E

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

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ACTCTCTGCT GTCGCCCGTC CCGCGCGCTC CTCGACCCG CTCGCTCCG CTCGCTCGG      60
CCCCGCGCGG CCCGTC AAC ATG ATC CGC TGC GGC CTG GCC TGC GAG CGC TGC      112
15          Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys
                1             5             10
CGC TGG ATC CTG CCC CTG CTC CTA CTC AGC GCC ATC GCC TTC GAC ATC      160
Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile
                15             20             25
20 ATC GCG CTG GCC GGC CGC GGC TGG TTG CAG TCT AGC GAC CAC GGC CAG      208
Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln
                30             35             40
ACG TCC TCG CTG TGG TGG AAA TGC TCC CAA GAG GGC GGC GGC AGC GGG      256
Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly
25          45             50             55
TCC TAC GAG GAG GGC TGT CAG AGC CTC ATG GAG TAC GCG TGG GGT AGA      304
Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg
        60             65             70             75
GCA GCG GCT GCC ATG CTC TTC TGT GGC TTC ATC ATC CTG GTG ATC TGT      352
30 Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys
                80             85             90
TTC ATC CTC TCC TTC TTC GCC CTC TGT GGA CCC CAG ATG CTT GTC TTC      400
Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe
                95             100             105
35 CTG AGA GTG ATT GGA GGT CTC CTT GCC TTG GCT GCT GTG TTC CAG ATC      448
Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Val Phe Gln Ile
                110             115             120
ATC TCC CTG GTA ATT TAC CCC GTG AAG TAC ACC CAG ACC TTC ACC CTT      496

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	Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu	
	125 130 135	
	CAT GCC AAC CGT GCT GTC ACT TAC ATC TAT AAC TGG GCC TAC GGC TTT	544
	His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe	
5	140 145 150 155	
	GGG TGG GCA GCC ACG ATT ATC CTG ATC GGC TGT GCC TTC TTC TTC TGC	592
	Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys	
	160 165 170	
	TGC CTC CCC AAC TAC GAA GAT GAC CTT CTG GGC AAT GCC AAG CCC AGG	640
10	Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg	
	175 180 185	
	TAC TTC TAC ACA TCT GCC TA ACTGGG AATGAATGTG GGAGAAAATC GCT	690
	Tyr Phe Tyr Thr Ser Ala	
	190	
15	GCTGCTGAGA TGGACTCCAG AAGAAGAAAC TGTTTCTCCA GGCGACTTTG AACCCATTTT	750
	TTGGCAGTGT TCATATTATT AAAC TAGTCA AAAATGCTAA AATAATTTGG GAGAAAAATAT	810
	TTTTTAAGTA GTGTTATAGT TTCATGTTTA TCITTTTATTA TGTTTTGTGA AGTTGTGTCT	870
	TTTCACTAAT TACCTATACT ATGCCAATAT TTCCTTATAT CTATCCATAA CATTTATACT	930
	ACATTTGTAA GAGAATATGC ACGTGAAACT TAACACTTTA TAAGGTAAAA ATGAGGTTTC	990
20	CAAGATTTAA TAATCTGATC AAGTTCCTGT TATTTCCTAAA TAGAATGGAC TTGGTCTGTT	1050
	AAGGGCTAAG GAGAAGAGGA AGATAAGGTT AAAAGTTGTT AATGACCAAA CATTCTAAAA	1110
	GAAATGCAAA AAAAAAGTTT ATTTTCAAGC CTTCGAAC TAAGGAAAA GC AAAATCAT	1170
	TTCCTAAATG CATATCATTT GTGAGAATTT CTCATTAATA TCCTGAATCA TTCATTTCAG	1230
	CTAAGGCTTC ATGTTGACTC GATATGTCAT CTAGGAAAGT ACTATTTCAT GGTCCAAACC	1290
25	TGTTGCCATA GTTGTAAGG CTTTCCTTTA AGTGTGAAAT ATTTAGATGA AATTTTCTCT	1350
	TTTAAAGTTC TTTATAGG GTAGGGTGTG GAAAAAGCTA TATTAATAAA TCTGTAGTGT	1410
	TTTGTGTTTA TATGTTTCTG ACCAGAGTAG ACTGGATTGA AAGATGGACT GGGTCTAATT	1470
	TATCATGACT GATAGATCTG GTTAAGTTGT GTAGTAAAGC ATTAGGAGG TCATTCTGT	1530
	CACAAAAGTG CCACTAAAC AGCCTCAGGA GAATAAATGA CTGCTTTTC TAAATCTCAG	1590
30	GTTTATCTGG GCTCTATCAT ATAGACAGGC TTCTGATAGT TTGCAACTGT AAGCAGAAAC	1650
	CTACATATAG TAAAAATCCT GGTCTTTCTT GGTAAACAGA TTTTAAATGT CTGATATAAA	1710
	ACATGCCACA GGAGAATTCG GGGATTGAG TTTCTCTGAA TAGCATATAT ATGATGCATC	1770
	GGATAGGTCA TTATGATTTT TTACCATTTT GACTTACATA ATGAAAACCA ATTCATTTTA	1830
	AATATCAGAT TATTATTTTG TAAGTTGTGG AAAAAAGCTAA TTGTAGTTTT CATTATGAAG	1890
35	TTTTCCTCAAT AAACCAGGTA TTCT	1914